

Patched-2 Antibodies

RELATED APPLICATIONS

This application is a continuation of USSN 09/293,505 filed 15 April 1999, now allowed, which claims priority under 35 U.S.C. § 119(e) to provisional application no. 60/081,884, filed 15 April 1998, all of which the entire disclosure is hereby incorporated by reference.

FIELD OF THE INVENTION

The present invention relates generally to signaling molecules, specifically to signaling and mediator molecules in the *hedgehog* (*Hh*) cascade which are involved in cell proliferation and differentiation.

BACKGROUND OF THE INVENTION

Development of multicellular organisms depends, at least in part, on mechanisms which specify, direct or maintain positional information to pattern cells, tissues, or organs. Various secreted signaling molecules, such as members of the transforming growth factor-beta (TGF- $\beta$ ), Wnt, fibroblast growth factors and hedgehog families have been associated with patterning activity of different cells and structures in *Drosophila* as well as in vertebrates. Perrimon, *Cell*: 80: 517-520 (1995).

Segment polarity genes were first discovered in *Drosophila*, which when mutated caused a change in the pattern of structures of the body segments. These changes affected the pattern along the head to tail axis. *Hedgehog* (*Hh*) was first identified as a segment-polarity gene by a genetic screen in *Drosophila melanogaster*, Nusslein-Volhard *et al.*, *Roux. Arch. Dev. Biol.* 193: 267-282 (1984), that plays a wide variety of developmental functions. Perrimon, *supra*. Although only one *Drosophila Hh* gene has been identified, three mammalian *Hh* homologues have been isolated: Sonic *Hh* (*Shh*), Desert *Hh* (*Dhh*) and Indian *Hh* (*Ihh*), Echelard *et al.*, *Cell* 75: 1417-30 (1993); Riddle *et al.*, *Cell* 75: 1401-16 (1993). *Shh* is expressed at high level in the notochord and floor plate of developing vertebrate embryos, and acts to establish cell fate in the developing limb, somites and neural tube. *In vitro* explant assays as well as ectopic expression of *Shh* in transgenic animals show that *SHh* plays a key role in neural tube patterning, Echelard *et al.* (1993), *supra*; Ericson *et al.*, *Cell* 81: 747-56 (1995); Marti *et al.*, *Nature* 375: 322-5 (1995); Roelink *et al.* (1995), *supra*; Hynes *et al.*, *Neuron* 19: 15-26 (1997). *Hh* also plays a role in the development of limbs (Krauss *et al.*, *Cell* 75: 1431-44 (1993); Laufer *et al.*, *Cell* 79, 993-1003 (1994)), somites (Fan and Tessier-Lavigne, *Cell* 79, 1175-86 (1994); Johnson *et al.*, *Cell* 79: 1165-73 (1994)), lungs (Bellusci *et al.*, *Develop.* 124: 53-63 (1997) and skin (Oro *et al.*, *Science* 276: 817-21 (1997)). Likewise, *Ihh* and *Dhh* are involved in bone, gut and germinal cell development, Apelqvist *et al.*, *Curr. Biol.* 7: 801-4 (1997); Bellusci *et al.*, *Dev. Suppl.* 124: 53-63 (1997); Bitgood *et al.*, *Curr. Biol.* 6: 298-304 (1996);

Roberts *et al.*, *Development* 121: 3163-74 (1995). Specifically, *Ihh* has been implicated in chondrocyte development [Vortkamp, A. *et al.*, *Science* 273: 613-22 (1996)] while *Dhh* plays a key role in testis development. Bitgood *et al.*, *supra*. With the exception of the gut, in which both *Ihh* and *Shh* are expressed, the expression patterns of the hedgehog family members do not overlap. Bitgood *et al.*, *supra*.

At the cell surface, Hh function appears to be mediated by a multicomponent receptor complex involving patched (*e.g.*, *Ptch*) and *Smoothed* (*e.g.*, *Smo*), two multi-transmembrane proteins initially identified as segment polarity genes in *Drosophila* and later characterized in vertebrates. Nakano *et al.*, *Nature* 341: 508-513 (1989); Goodrich *et al.*, *Genes Dev.* 10: 301-312 (1996); Marigo *et al.*, *Develop.* 122: 1225-1233 (1996); van den Heuvel, M. & Ingham, P.W., *Nature* 382: 547-551 (1996); Alcedo, J. *et al.*, *Cell* 86: 221-232 (1996); Stone, D.M. *et al.*, *Nature* 384: 129-34 (1996). Upon binding of *Hh* to *Patched*, the normal inhibitory effect of *Patched* on *Smo* is relieved, allowing *Smo* to transduce the *Hh* signal across the plasma membrane. It remains to be established if the *Patched/Smo* receptor complex mediates the action of all 3 mammalian hedgehogs or if specific components exist. Interestingly, a second murine *Patched* gene, *Patched-2* was recently isolated [Motoyama, J. *et al.*, *Nature Genetics* 18: 104-106 (1998)], but its function as a *Hh* receptor has not been established. In order to characterize *Patched-2* and compare it to *Patched* with respect to the biological function of the various *Hh* family members, Applicants have isolated the human *Patched-2* gene. Biochemical analysis of *Patched* and *Patched-2* show that both bind to all members of the *Hh* family with similar affinity and that both molecules can form a complex with *Smo*. However, the expression patterns of *Patched-2* and *Patched* do not overlap. While *Patched* is expressed throughout the mouse embryo, *Patched-2* is found mainly in spermatocytes which require Desert Hedgehog (*Dhh*) for proper development suggesting that *Patched-2* mediates *Dhh*'s activity in the testis. Chromosomal localization of *Patched-2* places it on chromosome 1p33-34, a region deleted in some germ cell tumors, raising the possibility that *Patched-2* may be a tumor suppressor in *Dhh* target cells.

## SUMMARY OF THE INVENTION

In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a *patched-2* polypeptide comprising the sequence of amino acids 1 to 1203 of Fig. 1 (SEQ ID NO:2), or (b) the complement of the DNA molecule of (a); and encoding a polypeptide having *patched-2* biological activity. The sequence identity preferably is > 91%, more preferably about 92%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least > 91%, preferably at least about 92%, and even more preferably at least about 95% sequence identity with a polypeptide having amino acid residues 1 to about 1203 of Fig. 1 (SEQ ID NO:2). In a further aspect, the isolated nucleic acid molecule comprises DNA encoding a human *patched-2* polypeptide having amino acid residues 1 to about 1203 of Fig. 1. In yet another aspect, the invention provides for an isolated nucleic acid comprising DNA having at least a 95% sequence identity to (a) a DNA molecule encoding the same mature polypeptide encoded by the

cDNA in ATCC Deposit No. 209778 (designation: pRK7.hptc2.Flag-1405), alternatively the coding sequence of clone pRK7.hptc2.Flag-1405, deposited under accession number ATCC 209778. In a still further aspect, the invention provides for a nucleic acid comprising human *patched-2* encoding sequence of the cDNA in ATCC Deposit No. 209778 (designation: pRK7.hptc2.Flag-1405) or a sequence which hybridizes thereto under stringent conditions.

In another embodiment, the invention provides a vector comprising DNA encoding a human *patched-2* polypeptide. A host cell comprising such a vector is also provided. By way of example, the host cells may be mammalian cells, (e.g. CHO cells), prokaryotic cells (e.g., *E. coli*) or yeast cells (e.g., *Saccharomyces cerevisiae*). A process for producing *patched-2* polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of *patched-2* and recovering the same from the cell culture.

In yet another embodiment, the invention provides an isolated *patched-2* polypeptide. In particular, the invention provides isolated native sequence *patched-2* polypeptide, which in one embodiment is a human *patched-2* including an amino acid sequence comprising residues 1 to about 1203 of Figure 1 (SEQ ID NO:2). Human *patched-2* polypeptides with or without the initiating methionine are specifically included. Alternatively, the invention provides a human *patched-2* polypeptide encoded by the nucleic acid deposited under accession number ATCC 209778.

In yet another embodiment, the invention provides chimeric molecules comprising a *patched-2* polypeptide fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises a *patched-2* polypeptide fused to an epitope tag sequence or a constant region of an immunoglobulin.

In yet another embodiment, the invention provides expressed sequence tag (EST) comprising the nucleotide sequences identified in Fig. 2A (905531) (SEQ ID NO:3) and Fig. 2B (1326258) (SEQ ID NO:5).

In yet another embodiment, the invention provides for alternatively spliced variants of human *patched-2* having *patched-2* biological activity.

In yet another embodiment, the invention provides for method of using *patched-2* for the treatment of disorders which are mediated at least in part by *Hedgehog* (*Hh*), especially *Desert hedgehog* (*Dhh*). In particular, testicular cancer. In yet another embodiment, the invention provides a method of using antagonists or agonists of *patched-2* for treating disorders or creating a desirable physiological condition effected by blocking *Hh* signaling, especially *Dhh* signaling. (E.g, contraception).

### **BRIEF DESCRIPTION OF THE DRAWINGS**

Figures 1A-1E shows the nucleotide (SEQ ID NO:1) and derived amino acid (SEQ ID NO:2) sequence of a native sequence of human *Ptch-2* polypeptide.

Figure 2A shows EST 905531 (SEQ ID NO:3) and Fig. 2B shows EST 1326258 (SEQ ID NO:5) in alignment with human *Ptch* (SEQ ID NO:18). These ESTs were used in the cloning of human full-length *Ptch*-

2 (SEQ ID NO:1).

Figures 3A-3D show a comparison between human *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2). Gaps introduced for optimal alignment are indicated by dashes. Identical amino acids are boxed. The 12 transmembrane domains are indicated by the gray boxes, all of which are conserved between the two sequences. Alignment results between the two sequences indicate 53% identity. The most significant difference is a shorter C-terminal intracellular domain in human *Ptch-2* (SEQ ID NO:2) in comparison with human *Ptch* (SEQ ID NO:4).

Figure 4 shows a northern blot of *Ptch-2* (SEQ ID NO:2) which indicates expression is limited to the testis. Multiple human fetal and adult tissue northern blots were probe fragments corresponding to the 3'-untranslated region of murine *Ptch-2*.

Figure 5 shows a chromosomal localization of two BAC clones which were isolated by PCR screening with human *patched-2* derived probes. Both probes were mapped by FISH to human chromosome 1p33-34.

Figures 6A-F is an *in situ* hybridization comparing *Ptch* (SEQ ID NO:4), *Ptch-2* (SEQ ID NO:2) and *Fused* (FuRK) (SEQ ID NO:10). High magnification of mouse testis showing expression of (A) *Ptch* (SEQ ID NO:4), *Ptch-2* (SEQ ID NO:2) (B) and FuRK (SEQ ID NO:10) (C). Low magnification of testis section hybridized with *Ptch-2* sense (SEQ ID NO:11) (D) and anti-sense probe (SEQ ID NO:12) (E) respectively. Fig. 6(F) shows low magnification of testis section hybridized with FuRK (SEQ ID NO:10). Scale bar: A, B, C: 0.05 mm; D, E, F: 0.33 mm.

Figure 7A is logarithmic plot comparing the binding *Ptch-2* (SEQ ID NO:2) to *Dhh* (SEQ ID NO:13) and *Shh* (SEQ ID NO:14). Competitive binding of recombinant murine <sup>125</sup>I-*Shh* to 293 cells overexpressing h*Ptch* (SEQ ID NO:4) or h*Ptch-2* (SEQ ID NO:2). There was no detectable binding to mock transfected cells (data not shown). Figure 7B is a western blot illustrating co-immunoprecipitation of epitope tagged *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) with epitope tagged *Smo* (SEQ ID NO:15). Immunoprecipitation was performed with antibodies to the Flag tagged *Ptch* (SEQ ID NO:4) and analyzed on a 6% acrylamide gel with antibodies to the Myc tagged *Smo* (SEQ ID NO:15). Protein complexes can be detected for both *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) with *Smo* (SEQ ID NO:15). *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) express at similar levels as shown by immunoprecipitation using antibodies to the Flag-tag and western blot using the same anti-Flag antibody.

Figures 8A-8D is a sequence comparison between human *Ptch-2* (SEQ ID NO:2) and murine *Ptch-2* (SEQ ID NO:7), which indicates that there is about 91% identity between the two sequences.

Figure 9 is an *in situ* hybridization which demonstrates the accumulation of *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) mRNA detected by *in situ* hybridization in basal cells of E18 transgenic mice overexpressing *SMO-M2* (SEQ ID NO: 16) (Xie *et al.*, *Nature* 391: 90-92 (1998).

Figures 10A-10D depict a partial sequence representing clone 3A (SEQ ID NO:8), a partial *patched-2* fragment which was initially isolated from a fetal brain library.

Figures 11A-B depict a partial sequence representing clone 16.1 (SEQ ID NO:9), a partial *patched-2*

fragment which isolated from a testis library.

## DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

### I. Definitions

The terms "*patched-2*" and "*patched-2* polypeptide" when used herein encompass native sequence *patched-2* and *patched-2* variants (which are further defined herein) having *patched-2* biological activity. *Patched-2* may be isolated from a variety of sources, such as from testes tissue types or from another source, or prepared by recombinant or synthetic methods.

A "native sequence *patched-2*" comprises a polypeptide having the same amino acid sequence as a human *patched-2* derived from nature. Such native sequence *patched-2* can be isolated from nature or can be produced by recombinant and/or synthetic means. The term "native sequence vertebrate *patched-2*" specifically encompasses naturally occurring truncated forms of human *patched-2*, naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of human *patched-2*. Thus, one embodiment of the invention, the native sequence *patched-2* is a mature or full-length native *patched-2* comprising amino acids 1 to 1203 of Fig. 1 (SEQ ID NO:2) with or without the initiating methionine at position 1.

"*Patched-2* variant" means an active human *patched-2* as defined below having at least > 91% amino acid sequence identity to (a) a DNA molecule encoding a *patched-2* polypeptide, or (b) the complement of the DNA molecule of (a). In a particular embodiment, the *patched-2* variant has at least > 91% amino acid sequence homology with the human *Ptch-2* (SEQ ID NO:2) having the deduced amino acid sequence shown in Fig. 1 for a full-length native sequence human *patched-2*. Such *patched-2* variants include, without limitation, *patched-2* polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the sequence of Fig. 1 (SEQ ID NO:2). Preferably, the nucleic acid or amino acid sequence identity is at least about 92%, more preferably at least about 93%, and even more preferably at least about 95%.

The term "*Ptch*" or "*Ptch-2*" refer to the particular species of molecules isolated and characterized in the application, while the terms "*patched*" and "*patched-2*" refer to the more generalized description as defined above.

"Percent (%) amino acid sequence identity" with respect to the *patched-2* sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the *patched-2* sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST-2 software that are set to their default parameters. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. Alternatively, % identity can be

determined by Align-2, authored by Genentech, Inc., which was filed with user documentation in the United States Copyright Office, Washington, D.C. 20559, on December 10, 1991, and is registered under U.S. Copyright Registration No. TXU 510087.

"Percent (%) nucleic acid sequence identity" with respect to the *patched-2* sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the *patched-2* sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST-2 software that are set to their default parameters. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. Alternatively, % identity can be determined by Align-2, authored by Genentech, Inc., which was filed with user documentation in the United States Copyright Office, Washington, D.C. 20559, on December 10, 1991, and is registered under U.S. Copyright Registration No. TXU 510087.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising *patched-2* polypeptide, or a portion thereof, *patched-2* to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the *patched-2* polypeptide. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 to about 50 amino acid residues (preferably, between about 10 to about 20 residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesin comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (*i.e.*, is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesins may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3 or IgG-4 subtypes, IgA (including IgA-1 and IgA-2, IgE, IgD or IgM. Immunoadhesion reported in the literature include fusions of the T cell receptor\* [Gascoigne *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 2936-2940 (1987)]; CD4\* [Capron *et al.*, *Nature* 337: 525-531 (1989); Traunecker *et al.*, *Nature* 339: 68-70 (1989); Zettmeissl *et al.*, *DNA Cell Biol. USA* 9: 347-353 (1990); Byrn *et al.*, *Nature* 344, 667-670 (1990)]; L-selectin (homing receptor) [Watson *et al.*, *J. Cell. Biol.* 110, 2221-2229 (1990); Watson *et al.*, *Nature* 349, 164-167 (1991)]; CD44\* [Aruffo *et al.*, *Cell* 61, 1303-1313 (1990)]; CD28\* and B7\* [Linsley *et al.*, *J. Exp. Med.* 173, 721-730 (1991)]; CTLA-4\* [Lisley *et al.*, *J. Exp. Med.* 174, 561-569 (1991)]; CD22\* [Stamenkovic *et al.*, *Cell* 66, 1133-1144 (1991)]; TNF receptor [Ashkenazi *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 10535-10539

(1991); Lesslauer *et al.*, *Eur. J. Immunol.* 27, 2883-2886 (1991); Peppel *et al.*, *J. Exp. Med.* 174, 1483-1489 (1991)]; NP receptors [Bennett *et al.*, *J. Biol. Chem.* 266, 23060-23067 (1991)]; IgE receptor  $\alpha$ -chain\* [Ridgway and Gorman, *J. Cell. Biol.* 115, abstr. 1448 (1991)]; HGF receptor [Mark, M.R. *et al.*, *J. Biol. Chem.*, 267(36): 26166-26171 (1992) ], where the asterisk (\*) indicates that the receptor is a member of the immunoglobulin superfamily.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends upon the ability of denatured DNA to reanneal when complementary strands are present in an environment near but below their  $T^m$  (melting temperature). The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. Moreover, stringency is also inversely proportional to salt concentrations. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, *Current Protocols in Molecular Biology* (1995).

"Stringent conditions," as defined herein may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50  $\mu$ g/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the vertebrate *patched-2* natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" *patched-2* nucleic acid molecule is a nucleic acid molecule that is identified and

separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the *patched-2* nucleic acid. An isolated *patched-2* nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated *patched-2* nucleic acid molecules therefore are distinguished from the corresponding native *patched-2* nucleic acid molecule as it exists in natural cells.

5 The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

10 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory  
15 leader, contiguous and in reading frame. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

20 The term "antibody" is used in the broadest sense and specifically covers single monoclonal antibodies (including agonist and antagonist antibodies), antibody compositions with polypeptidic specificity, as well as antibody fragments (*e.g.*, Fab, F(ab')<sub>2</sub> and Fv), so long as they exhibit the desired biological activity.

25 The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations that typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is  
30 not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler & Milstein, *Nature* 256:495 (1975), or may be made by recombinant DNA methods [see, *e.g.* U.S. Patent No. 4,816,567 (Cabilly *et al.*)].

35 The monoclonal antibodies herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the



remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity [U.S. Patent No. 4,816,567; Cabilly *et al.*; Morrison *et al.*, *Proc. Natl. Acad. Sci. USA* 81, 6851-6855 (1984)].

5 "Humanized" forms of non-human (*e.g.* murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-  
10 human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, corresponding non-human residues replace Fv framework residues of the human immunoglobulin. Furthermore, humanized antibody may comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications are made to further refine and optimize antibody performance. In general, the humanized antibody will comprise substantially all  
15 of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details see: Jones *et al.*, *Nature* 321, 522-525 (1986); Reichmann *et al.*, *Nature* 332, 323-329 (1988); Presta, *Curr. Op. Struct. Biol.* 2 593-596 (1992) and U.S. Patent No. 5,225,539 (Winter) issued July 6, 1993.  
20

"Active" or "activity" for the purposes herein refers to form(s) of *patched-2* which retain the biologic and/or immunologic activities of native or naturally occurring *patched-2*. A preferred activity is the ability to bind to and affect, *e.g.*, block or otherwise modulate, *hedgehog*, especially *Desert hedgehog* signaling. For example, the regulation of the pathogenesis of testicular cancer, male spermatocyte formation and basal cell  
25 carcinoma.

The term "antagonist" is used herein in the broadest sense to include any molecule which blocks, prevents, inhibits, neutralizes the normal functioning of *patched-2* in the *Hh* signaling pathway. One particular form of antagonist includes a molecule that interferes with the interaction between *Dhh* (SEQ ID NO:13) and *Ptch-2* (SEQ ID NO:2). Alternatively, an antagonist could also be a molecule which increases the levels of  
30 *patched-2*. In a similar manner, the term "agonist" is used herein to include any molecule which promotes, enhances or stimulates the binding of a *Hh* to *patched-2* in the *Hh* signaling pathway (*e.g.*, blocking binding of *Ptch-2* (SEQ ID NO:2) to *Smo* (SEQ ID NO:17)). Suitable molecules that affect the protein-protein interaction of *Hh* and *Ptch-2* and its binding proteins include fragments of the latter or small bioorganic molecules, *e.g.*, peptidomimetics, which will prevent or enhance, as the case may be, the binding of *Hh* to *Ptch-2*. Non-limiting  
35 examples include proteins, peptides, glycoproteins, glycopeptides, glycolipids, polysaccharides, oligosaccharides, nucleic acids, bioorganic molecules, peptidomimetics, pharmacological agents and their

metabolites, transcriptional and translation control sequences, and the like. Another preferred form of antagonist includes antisense oligonucleotides that inhibit proper transcription of wild type *patched-2*.

The term "modulation" or "modulating" means upregulation or downregulation of a signaling pathway. Cellular processes under the control of signal transduction may include, but are not limited to, transcription of specific genes; normal cellular functions, such as metabolism, proliferation, differentiation, adhesion, apoptosis and survival, as well as abnormal processes, such as transformation, blocking of differentiation and metastasis.

The techniques of "polymerase chain reaction," or "PCR", as used herein generally refers to a procedure wherein minute amounts of a specific piece of nucleic acid, RNA and/or DNA are amplified as described in U.S. Pat. No. 4,683,195 issued 28 July 1987. Generally, sequence information from the ends of the region of interest or beyond needs to be available, such that oligonucleotide primers can be designed; these primers will be identical or similar in sequence to opposite strands of the template to be amplified. The 5' terminal nucleotides of the two primers may coincide with the ends of the amplified material. PCR sequences form total genomic DNA, and cDNA transcribed from total cellular RNA, bacteriophage, or plasmid sequences, etc. See generally Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.* 51: 263 (1987); Erlich, Ed., PCR Technology, (Stockton Press, NY, 1989). As used herein, PCR is considered to be one, but not the only, example of a nucleic acid test sample comprising the use of a known nucleic acid as a primer and a nucleic acid polymerase to amplify or generate a specific piece of nucleic acid.

## II. Compositions and Methods of the Invention

### A. Full-length *patched-2*

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as *patched-2*. In particular, Applicants have identified and isolated cDNA encoding a human *patched-2* polypeptide, as disclosed in further detail in the Examples below. Using BLAST, BLAST-2 and FastA sequence alignment computer programs (set to the default parameters), Applicants found that a full-length native sequence human *Ptch-2* (SEQ ID NO:2) (shown in Figure 3) has 53% amino acid sequence identity with human *patched* (SEQ ID NO:4). Moreover human full-length *patched-2* (SEQ ID NO:2) has about a 91% sequence identity with murine *Ptch-2* (SEQ ID NO:7) (Fig. 8). Accordingly, it is presently believed that the human *patched-2* (SEQ ID NO:2) disclosed in the present application is a newly identified member of the mammalian hedgehog signaling cascade, specifically *Desert hedgehog*.

The full-length native sequence of human *patched-2* gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length gene or to isolate still other vertebrate homolog genes (for instance, those encoding naturally-occurring variants of *patched-2* or *patched-2* from other species) which have a desired sequence identity to the human *patched-2* sequence disclosed in Fig.1 (SEQ ID NO:2). Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the nucleotide sequence of Fig. 1 (SEQ ID NO:1) or from genomic sequences including promoters, enhancer elements and introns of native sequence vertebrate *patched-2*. By way of example, a

screening method will comprise isolating the coding region of the vertebrate *patched-2* gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as  $^{32}\text{P}$  or  $^{35}\text{S}$ , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the vertebrate *patched-2* gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to.

#### B. Patched-2 Variants

In addition to the full-length native sequence *patched-2* described herein, it is contemplated that *patched-2* variants can be prepared. *Patched-2* variants can be prepared by introducing appropriate nucleotide changes into a known *patched-2* DNA, or by synthesis of the desired *patched-2* polypeptides. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of *patched-2*.

Variations in the native full-length sequence *patched-2* or in various domains of the *patched-2* described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the *patched-2* that results in a change in the amino acid sequence of *patched-2* as compared with the native sequence *patched-2*. Optionally, the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of *patched-2*. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the *patched-2* with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, *i.e.*, conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity in the *in vitro* assay described in the Examples below.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter *et al.*, *Nucl. Acids Res.*, 13:4331 (1986); Zoller *et al.*, *Nucl. Acids Res.*, 10: 6487 (1987)], cassette mutagenesis [Wells *et al.*, *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells *et al.*, *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the vertebrate *patched-2* variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino

acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, *The Proteins*, (W.H. Freeman & Co., N.Y.); Chothia, *J. Mol. Biol.*, 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

In the comparison between human *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) sequences depicted in Figure 3, the 12 transmembrane domains are identified in gray, while identical residues are boxed. Gaps are indicated by dashes (-) and are inserted to maximize the total identity score between the two sequences.

### C. Modifications of *patched-2*

Covalent modifications of *patched-2* are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of *patched-2* with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the vertebrate *patched-2*. Derivatization with bifunctional agents is useful, for instance, for crosslinking *patched-2* to a water-insoluble support matrix or surface for use in the method for purifying anti-*patched-2* antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazo-acetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azido-salicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis-(succinimidyl-propionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)-dithio]propionimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of *patched-2* comprises linking the *patched-2* polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. Such modifications would be expected to increase the half-life of the molecules in circulation in a mammalian system; Extended half-life of *patched-2* molecules might be useful under certain circumstances, such as where the *patched-2* variant is administered as a therapeutic agent.

The *patched-2* of the present invention may also be modified in a way to form a chimeric molecule comprising *patched-2* bonded to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of *patched-2* with a tag polypeptide, which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the *patched-2*. The presence of such epitope-tagged forms of the *patched-2* can be

detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the *patched-2* to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of the *patched-2* with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule. Ordinarily, the C-terminus of a contiguous amino acid sequence of a *patched-2* receptor is fused to the N-terminus of a contiguous amino acid sequence of an immunoglobulin constant region, in place of the variable region(s), however N-terminal fusions are also possible.

Typically, such fusions retain at least functionally active hinge, CH2 and CH3 domains of the constant region of an immunoglobulin heavy chain. Fusions are also made to the C-terminus of the Fc portion of a constant domain, or immediately N-terminal to the CH1 of the heavy chain or the corresponding region of the light chain. This ordinarily is accomplished by constructing the appropriate DNA sequence and expressing it in recombinant cell culture. Alternatively, immunoadhesins may be synthesized according to known methods.

The precise site at which the fusion is made is not critical; particular sites are well known and may be selected in order to optimize the biological activity, secretion or binding characteristics of the immunoadhesins.

In a preferred embodiment, the C-terminus of a contiguous amino acid sequence which comprises the binding site(s) of *patched-2*, at the N-terminal end, to the C-terminal portion of an antibody (in particular the Fc domain), containing the effector functions of an immunoglobulin, *e.g.*, immunoglobulin G<sub>1</sub> (IgG-1). As herein above mentioned, it is possible to fuse the entire heavy chain constant region to the sequence containing the binding site(s). However, more preferably, a sequence beginning in the hinge region just upstream of the papain cleavage site (which defines IgG Fc chemically; residue 216, taking the first residue of heavy chain constant region to be 114 [Kobayashi *et al.*, *supra*], or analogous sites of other immunoglobulins) is used in the fusion. Although it was earlier thought that in immunoadhesins the immunoglobulin light chain would be required for efficient secretion of the heterologous protein-heavy chain fusion proteins, it has been found that even the immunoadhesins containing the whole IgG1 heavy chain are efficiently secreted in the absence of light chain. Since the light chain is unnecessary, the immunoglobulin heavy chain constant domain sequence used in the construction of the immunoadhesins of the present invention may be devoid of a light chain binding site. This can be achieved by removing or sufficiently altering immunoglobulin heavy chain sequence elements to which the light chain is ordinarily linked so that such binding is no longer possible. Thus, the CH1 domain can be entirely removed in certain embodiments of the *patched-2*/immunoglobulin chimeras.

In a particularly preferred embodiment, the amino acid sequence containing the extracellular domain(s) of *patched-2* is fused to the hinge region and CH2, CH3; or CH1, hinge, CH2 and CH3 domains of an IgG-1, IgG-2, IgG-3, or IgG-4 heavy chain.

In some embodiments, the *patched-2*/immunoglobulin molecules (immunoadhesins) are assembled as monomers, dimers or multimers, and particularly as dimers or tetramers. Generally, these assembled immunoadhesins will have known unit structures similar to those of the corresponding immunoglobulins. A basic

four chain structural unit (a dimer of two immunoglobulin heavy chain-light chain pairs) is the form in which IgG, IgA and IgE exist. A four chain unit is repeated in the high molecular weight immunoglobulins; IgM generally exists as a pentamer of basic four-chain units held together by disulfide bonds. IgA globulin, and occasionally IgG globulin, may also exist in a multimeric form in serum. In the case of multimers, each four chain unit may be the same or different.

It is not necessary that the entire immunoglobulin portion of the *patched-2*/immunoglobulin chimeras be from the same immunoglobulin. Various portions of different immunoglobulins may be combined, and variants and derivatives of native immunoglobulins can be made as herein above described with respect to *patched-2*, in order to optimize the properties of the immunoadhesin molecules. For example, immunoadhesin constructs in which the hinge of IgG-1 was replaced with that of IgG-3 were found to be functional and showed pharmacokinetics comparable to those of immunoadhesins comprising the entire IgG-1 heavy chain.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field *et al.*, *Mol. Cell. Biol.*, 8: 2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan *et al.*, *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky *et al.*, *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp *et al.*, *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin *et al.*, *Science*, 255:192-194 (1992)]; an  $\alpha$ -tubulin epitope peptide [Skinner *et al.*, *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)]. A preferred tag is the influenza HA tag.

#### D. Preparation of *patched-2*

The description below relates primarily to production of a particular *patched-2* by culturing cells transformed or transfected with a vector containing *patched-2* nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare *patched-2*. For instance, the *patched-2* sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, *e.g.*, Stewart *et al.*, *Solid-Phase Peptide Synthesis*, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the vertebrate *patched-2* may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length *patched-2*.

##### 1. Isolation of DNA encoding vertebrate *patched-2*

DNA encoding *patched-2* may be obtained from a cDNA library prepared from tissue believed to possess the *patched-2* mRNA and to express it at a detectable level. Accordingly, human *patched-2* DNA can

be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples.

The vertebrate *patched-2*-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to the *patched-2* or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding vertebrate *patched-2* is to use PCR methodology [Sambrook *et al.*, *supra*; Dieffenbach *et al.*, *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook *et al.*, *supra*.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs such as BLAST, BLAST-2, ALIGN, DNASTar, and INHERIT which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook *et al.*, *supra*, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

## 2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for *patched-2* production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: A Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook *et al.*, *supra*.

Methods of transfection are known to the ordinarily skilled artisan, for example, CaPO<sub>4</sub> and

electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook *et al.*, *supra*, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw *et al.*, *Gene*, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology* 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen *et al.*, *J. Bact.*, 130:946 (1977) and Hsiao *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown *et al.*, *Methods in Enzymology*, 185:527-537 (1990) and Mansour *et al.*, *Nature*, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635).

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for vertebrate *patched-2*-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism.

Suitable host cells for the expression of vertebrate *patched-2* are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, *J. Gen Virol.*, 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

### 3. Selection and Use of a Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding *patched-2* may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an



appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques, which are known to the skilled artisan.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 $\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. A preferred replicable expression vector is the plasmid pRK5. *Holmes et al., Science*, 253:1278-1280 (1991).

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the *patched-2* nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub *et al., Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb *et al., Nature*, 282:39 (1979); Kingsman *et al., Gene*, 7:141 (1979); Tschemper *et al., Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the *patched-2* nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter systems [Chang *et al., Nature*, 275:615 (1978); Goeddel *et al., Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer *et al., Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding *patched-2*.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman *et al., J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess *et al., J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phospho-fructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase,

phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

*Patched-2* transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Inserting an enhancer sequence into the vector may increase transcription of a DNA encoding the vertebrate *patched-2* by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the *patched-2* coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding *patched-2*.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of *patched-2* in recombinant vertebrate cell culture are described in Gething *et al.*, *Nature*, 293:620-625 (1981); Mantei *et al.*, *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

#### 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA

hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence *patched-2* polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence *patched-2* to *patched-2* DNA and encoding a specific antibody epitope.

#### 5. Purification of Polypeptide

Forms of *patched-2* may be recovered from host cell lysates. Since *patched-2* is membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of *patched-2* can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify *patched-2* from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the *patched-2*. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular *patched-2* produced.

#### E. Uses for *patched-2*

##### (1) *Patched-2 is a specific receptor for Dhh*

The *hedgehog* signaling pathway has been implicated in the formation of embryonic structures in mammals and invertebrates. The multi-pass transmembrane receptor *Ptch*, is a negative regulator of the *hedgehog* pathway, repressing the serpentine signaling molecule *Smoothed* (*Smo*). Data have shown that loss of *Ptch* leads to deregulation of the *hedgehog* pathway leading to formation of aberrant structures in the embryos and carcinoma in the adult.

Applicants' newly identified second human *patched* gene, termed *patched-2*, has a similar 12 transmembrane domain topology as does *patched*, and can bind to all the members of the *Hh* family and can

complex with *Smo* (SEQ ID NO:17). However, the expression patterns of *Ptch-2* and *Ptch* do not overlap. *Ptch-2* is expressed mainly in the developing spermatocytes, which are supported directly by the *Dhh* producing Sertoli cells, which suggests that *Ptch-2* is a receptor for Desert hedgehog.

In the adult tubule, Sertoli cells, which are unusually large secretory cells, traverse the seminiferous tubule from the basal lamina to the luminal aspect, sending out cytoplasmic protrusions that engulf the germ cells. These contacts are particularly close during spermiogenesis, in which the haploid round spermatids undergo differentiation to produce the highly specialized, motile sperm. Tight junctions between adjacent Sertoli cells compartmentalize the tubule into a basal region, which contains mitotic spermatogonia and early spermatocytes, and an adluminal compartment, which contains meiotic spermatocytes and maturing spermatids. In fact, a Sertoli-derived cell line supports the meiotic progression of germ cells in culture, consistent with the view that factors derived from Sertoli cells contribute to germ cell maturation, Rassoulzadegan, M., *et al.*, *Cell* 1993, 75: 997-1006. Loss of *Dhh* activity results in a recessive, sex-specific phenotype. Female mice homozygous for the mutation were fully viable and fertile, whereas male mice were viable but infertile. A gross examination indicated that, as early as 18.5 dpc, the testes of mutant males were noticeably smaller than those of heterozygous littermates. Bitgood *et al.*, *Curr. Biol.*, 1996 6(3): 298-304. Thus, Sertoli cells likely independently regulate mitotic and meiotic stages of germ cell development during postnatal development. Therefore, since patched-2 appears to be the receptor for *Dhh* (SEQ ID NO:13), molecules which modulate the binding of *Dhh* (SEQ ID NO:13) to *Ptch-2* would affect the activation of *Dhh* signaling, and thereby would have utility in the treatment of conditions which are modulated by *Dhh* (SEQ ID NO:13). (For example, testicular cancer). Alternatively, it is also provided that antagonists or agonists of *patched-2* may be used for treating disorders or creating a desirable physiological condition effected by blocking *Dhh* (SEQ ID NO:13) signaling. (E.g, contraception, infertility treatment).

## (2) General uses for *patched-2*

Nucleotide sequences (or their complement) encoding *patched-2* have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. *Patched-2* nucleic acid will also be useful for the preparation of *patched-2* polypeptides by the recombinant techniques described herein.

The full-length native sequence *patched-2* gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length gene or to isolate still other genes (for instance, those encoding naturally-occurring variants of *patched-2*) which have a desired sequence identity to the *patched-2* sequence disclosed in Fig. 1 (SEQ ID NO:1). Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the nucleotide sequence of Fig. 1 (SEQ ID NO:1) or from genomic sequences including promoters, enhancer elements and introns of native sequence *patched-2*. By way of example, a screening method will comprise isolating the coding region of the *patched-2* gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled

by a variety of labels, including radionucleotides such as <sup>32</sup>P or <sup>35</sup>S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the *patched-2* gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine to which members of such libraries the probe hybridizes.

5 Hybridization techniques are described in further detail in the Examples below.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related *patched-2* sequences.

Nucleotide sequences encoding *patched-2* can also be used to construct hybridization probes for mapping the gene, which encodes *patched-2* and for the genetic analysis of individuals with genetic disorders.

10 The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

*Patched-2* polypeptides can be used in assays to identify the other proteins or molecules involved in complexing with *patched-2* which ultimately results in the modulation of hedgehog signaling. Alternatively, these molecules can modulate the binding of *patched-2* to *Dhh* (SEQ ID NO:13). By such methods, inhibitors of the binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the substrate of *patched-2* can be used to isolate correlative complexing proteins. Screening assays can be designed to find lead compounds that mimic the biological activity of a native *patched-2* or to find those that act as a substrate for *patched-2*. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Such small molecule inhibitors could block the enzymatic action of *patched-2*, and thereby inhibit *hedgehog* signaling. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode *patched-2* or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (*e.g.*, a mouse or rat) is an animal having cells that contain a transgene, was introduced into the animal or an ancestor of the animal at a prenatal, *e.g.*, an embryonic stage.

30 A transgene is a DNA sequence that is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding *patched-2* can be used to clone genomic DNA encoding *patched-2* in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding *patched-2*. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for *patched-2* transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene

encoding *patched-2* introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding *patched-2*. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression.

5 Non-human homologues of vertebrate *patched-2* can be used to construct a *patched-2* "knock out" animal which has a defective or altered gene encoding *patched-2* as a result of homologous recombination between the endogenous gene encoding *patched-2* and altered genomic DNA encoding *patched-2* introduced into an embryonic cell of the animal. For example, cDNA encoding *patched-2* can be used to clone genomic DNA encoding *patched-2* in accordance with established techniques. A portion of the genomic DNA encoding  
10 *patched-2* can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see *e.g.*, Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see  
15 *e.g.*, Li *et al*, *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse or rat) to form aggregation chimeras [see *e.g.*, Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be  
20 identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the *patched-2* polypeptide.

Suppression or inhibition (antagonism) of *Dhh* signaling is also an objective of therapeutic strategies.  
25 Since *patched-2* can combine with all members of the hedgehog family (*i.e.*, *Shh*, *Dhh*, *Ihh*), antagonist molecules which prevent the binding of hedgehog molecules to *Ptch-2* (SEQ ID NO:2) have therapeutic utility. For example, *Shh* signaling is known to be activated in Basal Cell Carcinoma; *Dhh* (SEQ ID NO:13) is known to be involved in the regulation of spermatogenesis. Inhibitor or antagonist of *Hh* signaling would be effective therapeutics in the treatment of Basal Cell Carcinoma or male contraception, respectively.

30 The stimulation of *Dhh* signaling (agonism) is also an objective of therapeutic strategies. Since *Ptch-2* (SEQ ID NO:2) also binds to the other members of the *Hh* family, *Ihh* and *Shh*, activating *Dhh* signaling would be useful in disease states or disorders characterized by inactive or insufficient *Hh* signaling. For example, degenerative disorders of the nervous system, *e.g.*, Parkinson's disease, memory deficits, Alzheimer's disease, Lou Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug addiction. Additionally, *patched-2*  
35 agonists could be used to treat gut diseases, bone diseases, skin diseases, diseases of the testis (including infertility), ulcers, lung diseases, diseases of the pancreas, diabetes, osteoporosis.

F. Anti-patched-2 Antibodies

The present invention further provides anti- vertebrate *patched-2* antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The anti-*patched-2* antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the *patched-2* polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants that may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

2. Monoclonal Antibodies

The anti-*patched-2* antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the *patched-2* polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against *patched-2*. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison *et al.*, *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well



known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

*In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

### 3. Humanized Antibodies

The anti-*patched-2* antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones *et al.*, *Nature*, 321:522-525 (1986); Riechmann *et al.*, *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones *et al.*, *Nature*, 321:522-525 (1986); Riechmann *et al.*, *Nature*, 332:323-327 (1988); Verhoeven, *et al.*, *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage

display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks *et al.*, *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner *et al.*, *J. Immunol.*, 147(1):86-95 (1991)).

#### 4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the vertebrate *patched-2*, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

#### 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

G. Uses for anti-*patched-2* Antibodies

The anti-*patched-2* antibodies of the invention have various utilities. For example, anti-*patched-2* antibodies may be used in diagnostic assays for *patched-2*, e.g., detecting its expression in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter *et al.*, *Nature*, 144: 945 (1962); David *et al.*, *Biochemistry*, 13:1014 (1974); Pain *et al.*, *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

Anti-*patched-2* antibodies also are useful for the affinity purification of *patched-2* from recombinant cell culture or natural sources. In this process, the antibodies against *patched-2* are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the *patched-2* to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the *patched-2*, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the *patched-2* from the antibody.

Basal cell carcinoma (BCC) is the most common human cancer. The *Hh* signaling pathway was found to activated in all BCCs. Loss of *Ptch* function is thought to lead to unregulated *Smo* activity and is responsible for about half of all BCCs. *Ptch* being a target of the *Hh* pathway itself, increases in *Ptch* mRNA levels have been detected in BCC [Galiani, *et al.*, *Nature Genet.* 14: 78-81 (1996)] as well as in animal models of BCC. Oro *et al.*, *Science* 276: 817-821 (1997); Xie *et al.*, *Nature* 391: 90-92 (1998). Abnormal activation of *Sh* signaling, such as that which occurs in BCC, was examined to confirm whether *Ptch-2* (SEQ ID NO:2) expression was increased. As shown in Fig. 9, an *in situ* hybridization for *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) in *Smo*-M2 (SEQ ID NO:16) transgenic mice (Xie *et al.*, *supra*), while lower than *Ptch*, was still high in tumor cells. This suggests that therapeutic antibodies directed toward *Ptch-2* (SEQ ID NO:2) may be useful for the treatment of BCC.

Anti-*patched-2* antibodies also have utilities similar to those articulated for under the previous section "E. Uses of Patched-2". Depending on whether anti-*patched-2* antibodies will bind *patched-2* receptors so as to either inhibit *Hh* signaling (antagonist) or inhibit *patched-2* complexing with *Smo* (SEQ ID NO:17) and thereby remove the normal inhibitory effect of *Smo* (SEQ ID NO:17) on *Hh* signaling (agonist) the antibody

will have utilities corresponding to those articulated previously for *patched-2*.

#### H. Patched-2 Antagonists

Several approaches may be suitably employed to create the *patched-2* antagonist and agonist compounds of the present invention. Any approach where the antagonist molecule can be targeted to the interior of the cell, which interferes or prevents wild type *patched-2* from normal operation is suitable. For example, competitive inhibitors, including mutant *patched-2* receptors which prevent wild type *patched-2* from properly binding with other proteins necessary for *Dhh* and *Hh* signaling. Additional properties of such antagonist or agonist molecules are readily determinable by one of ordinary skill, such as size, charge and hydrophobicity suitable for transmembrane transport.

Where mimics or other mammalian homologues of *patched-2* are to be identified or evaluated, the cells are exposed to the test compound and compared to positive controls which are exposed only to human *patched-2*, and to negative controls which were not exposed to either the compound or the natural ligand. Where antagonists or agonists of *patched-2* signal modulation are to be identified or evaluated, the cells are exposed to the compound of the invention in the presence of the natural ligand and compared to controls which are not exposed to the test compound.

Detection assays may be employed as a primary screen to evaluate the *Hh* signaling inhibition/enhancing activity of the antagonist/agonist compounds of the invention. The assays may also be used to assess the relative potency of a compound by testing a range of concentrations, in a range from 100 mM to 1 pM, for example, and computing the concentration at which the amount of phosphorylation or signal transduction is reduced or increased by 50% (IC<sub>50</sub>) compared to controls.

Assays can be performed to identify compounds that affect *Hh* signaling of *patched-2* substrates. Specifically, assays can be performed to identify compounds that increase the phosphorylation activity of *patched-2* or assays can be performed to identify compounds that decrease the *Hh* signaling of *patched-2* substrates. These assays can be performed either on whole cells themselves or on cell extracts. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, cell based assays, etc. Such assay formats are well known in the art.

The screening assays of the present invention are amenable to high-throughput screening of chemical libraries, and are particularly suitable for identifying small molecule drug candidates.

#### (1) Antagonist and agonist molecules

To screen for antagonists and/or agonists of *patched-2* signaling, the assay mixture is incubated under conditions whereby, but for the presence of the candidate pharmacological agent, *patched-2* induces hedgehog signaling with a reference activity. The mixture components can be added in any order that provides for the requisite hedgehog activity. Incubation may be performed at any temperature that facilitates optimal binding, typically between about 4° and 40°C, more commonly between about 15° and 40°C. Incubation periods are

likewise selected for optimal binding but also minimized to facilitate rapid, high-throughput screening, and are typically between about 0.1 and 10 hours, preferably less than 5 hours, more preferably less than 2 hours. After incubation, the effect of the candidate pharmacological agent on the *patched-2* signaling is determined in any convenient way. For cell-free binding-type assays, a separation step is often used to separate bound and unbound components. Separation may, for example, be effected by precipitation (*e.g.* TCA precipitation, immunoprecipitation, *etc.*), immobilization (*e.g.* on a solid substrate), followed by washing. The bound protein is conveniently detected by taking advantage of a detectable label attached to it, *e.g.* by measuring radioactive emission, optical or electron density, or by indirect detection using, *e.g.* antibody conjugates.

For example, a method of screening for suitable *patched-2* antagonists and/or agonists could involve the application of *Dhh* and other hedgehog ligands. Such a screening assay could compare *in situ* hybridization in the presence and absence of the candidate antagonist and/or agonist in a *patched-2* expressing tissue as well as confirmation or absence of *patched-2* modulated cellular development. Typically these methods involve exposing an immobilized *patched-2* to a molecule suspected of binding thereto and determining the level of ligand binding downstream activation of reporter constructs and/or evaluating whether or not the molecule activates (or blocks activation of) *patched-2*. In order to identify such *patched-2* binding ligands, *patched-2* can be expressed on the surface of a cell and used to screen libraries of synthetic candidate compounds or naturally-occurring compounds (*e.g.*, from endogenous sources such as serum or cells).

Suitable molecules that affect the protein-protein interaction of *patched-2* and its binding proteins include fragments of the latter or small molecules, *e.g.*, peptidomimetics, which will inhibit ligand-receptor interaction. Such small molecules, which are usually less than 10 K molecular weight, are preferable as therapeutics since they are more likely to be permeable to cells, are less susceptible to degradation by various cellular mechanisms, and are not as apt to elicit an immune response as proteins. Small molecules include but are not limited to synthetic organic or inorganic compounds. Many pharmaceutical companies have extensive libraries of such molecules, which can be conveniently screened by using the assays of the present invention. Non-limiting examples include proteins, peptides, glycoproteins, glycopeptides, glycolipids, polysaccharides, oligosaccharides, nucleic acids, bioorganic molecules, peptidomimetics, pharmacological agents and their metabolites, transcriptional and translation control sequences, and the like.

A preferred technique for identifying molecules which bind to *patched-2* utilizes a chimeric substrate (*e.g.*, epitope-tagged *patched-2* or *patched-2* immunoadhesin) attached to a solid phase, such as the well of an assay plate. The binding of the candidate molecules, which are optionally labeled (*e.g.*, radiolabeled), to the immobilized receptor can be measured. Alternatively, competition for various *Hh* pathways, especially *Dhh* (SEQ ID NO:13) can be measured. In screening for antagonists and/or agonists, *patched-2* can be exposed to a *patched-2* substrate followed by the putative antagonist and/or agonist, or the *patched-2* binding protein and antagonist and/or agonist can be added simultaneously, and the ability of the antagonist and/or agonist to block *patched-2* activation can be evaluated.

(2) *Detection assays*

The *patched-2* polypeptides are useful in assays for identifying lead compounds for therapeutically active agents that modulate *patched-2* receptor/ligand hedgehog signaling. Specifically, lead compounds that either prevent the formation of *patched-2* signaling complexes or prevent or attenuate *patched-2* modulated hedgehog signaling (e.g., binding to *patched-2*) can be conveniently identified.

Various procedures known in the art may be used for identifying, evaluating or assaying the inhibition of activity of the *patched-2* proteins of the invention. As *patched-2* is believed to be a receptor for *Dhh* (SEQ ID NO:13), but also binds *Shh* (SEQ ID NO:14) and *Ihh* (SEQ ID NO:29), techniques known for use with identifying ligand/receptor modulators may also be employed with the present invention. In general, such assays involve exposing target cells in culture to the compounds and a) biochemically analyzing cell lysates to assess the level and/or identity of binding; or (b) scoring phenotypic or functional changes in treated cells as compared to control cells that were not exposed to the test substance. Such screening assays are described in U.S.P. 5,602,171, U.S.P. 5,710,173, WO 96/35124 and WO 96/40276.

(a) *Biochemical detection techniques*

Biochemical analysis can be evaluated by a variety of techniques. One typical assay mixture which can be used with the present invention contains *patched-2* and a ligand protein with which *patched-2* is normally associated (e.g., *Dhh* (SEQ ID NO:13)) usually in an isolated, partially pure or pure form. One or both of these components may be *patched-2* to another peptide or polypeptide, which may, for example, provide or enhance protein-protein binding, improve stability under assay conditions, etc. In addition, one of the components usually comprises or is coupled to a detectable label. The label may provide for direct detection by measuring radioactivity, luminescence, optical or electron density, etc., or indirect detection such as an epitope tag, an enzyme, etc. The assay mixture can additionally comprise a candidate pharmacological agent, and optionally a variety of other components, such as salts, buffers, carrier proteins, e.g. albumin, detergents, protease inhibitors, nuclease inhibitors, antimicrobial agents, etc., which facilitate binding, increase stability, reduce non-specific or background interactions, or otherwise improve the efficiency or sensitivity of the assay.

The following detection methods may also be used in a cell-free system wherein cell lysate containing the signal transducing substrate molecule and *patched-2* is mixed with a compound of the invention. To assess the activity of the compound, the reaction mixture may be analyzed by the SDS-PAGE technique or it may be added to substrate-specific anchoring antibody bound to a solid support, and a detection procedure as described above is performed on the separated or captured substrate to assess the presence or absence of a *patched-2* binding ligand. The results are compared to those obtained with reaction mixtures to which the compound is not added. The cell-free system does not require the natural ligand or knowledge of its identity. For example, Posner *et al.* (U.S.P. 5,155,031 describes the use of insulin receptor as a substrate and rat adipocytes as target cells to demonstrate the ability of pervanadate to inhibit PTP activity. Another example, Burke *et al.*, *Biochem.*

*Biophys. Res. Comm.* 204: 129-134 (1994) describes the use of autophosphorylated insulin receptor and recombinant PTP1B in assessing the inhibitory activity of a phosphotyrosyl mimetic.

(i) *Whole cell detection*

A common technique involves incubating cells with *patched-2* and radiolabeled ligand, lysing the cells, separating cellular protein components of the lysate using an SDS-polyacrylamide gel (SDS-PAGE) technique, in either one or two dimensions, and detecting the presence of labeled proteins by exposing X-ray film. Detection can also be effected without using radioactive labeling. In such a technique, the protein components (*e.g.*, separated by SDS-PAGE) are transferred to a nitrocellulose membrane where the presence of patched-ligand complexes is detected using an anti-ligand antibody.

Alternatively, the anti-*patched-2* ligand antibody can be conjugated with an enzyme, such as horseradish peroxidase, and detected by subsequent addition of a colorimetric substrate for the enzyme. A further alternative involves detecting the anti-*patched-2* ligand by reacting with a second antibody that recognizes anti-*patched-2* ligand, this second antibody being labeled with either a radioactive moiety or an enzyme as previously described. Examples of these and similar techniques are described in Hansen *et al.*, *Electrophoresis* 14: 112-126 (1993); Campbell *et al.*, *J. Biol. Chem.* 268: 7427-7434 (1993); Donato *et al.*, *Cell Growth Diff.* 3: 258-268 (1992); Katagiri *et al.*, *J. Immunol.* 150: 585-593 (1993). Additionally, the anti-*patched-2* ligand can be detected by labeling it with a radioactive substance, followed by scanning the labeled nitrocellulose to detect radioactivity or exposure of X-ray film.

Further detection methods may be developed which are preferred to those described above. Especially for use in connection with high-throughput screening, it is expected that such methods would exhibit good sensitivity and specificity, extended linear range, low background signal, minimal fluctuation, compatibility with other reagents, and compatibility with automated handling systems.

The *in vivo* efficacy of the treatment of the present invention can be studied against chemically induced tumors in various rodent models. Tumor cell lines propagated in *in vitro* cell cultures can be introduced in experimental rodents, *e.g.* mice by injection, for example by the subcutaneous route. Techniques for chemical inducement of tumors in experimental animals are well known in the art.

(ii) *Kinase assays*

Because *patched-2* is a negative regulator of *Hh* signaling, which when activated by *Hh* releases the normal inhibitory effect on *Smo*, the inhibition of *patched-2* binding to *Smo* can be measured by activation of various kinase substrate associated with *Hh* signaling. When the screening methods of the present invention for *patched-2* antagonists/agonists are carried out as an *ex vivo* assay, the target kinase (*e.g. fused*) can be a substantially purified polypeptide. The kinase substrate (*e.g.*, MBP, *Gli*) is a substantially purified substrate, which in the assay is phosphorylated in a reaction with a substantially purified phosphate source that is

catalyzed by the kinase. The extent of phosphorylation is determined by measuring the amount of substrate phosphorylated in the reaction. A variety of possible substrates may be used, including the kinase itself in which instance the phosphorylation reaction measured in the assay is autophosphorylation. Exogenous substrates may also be used, including standard protein substrates such as myelin basic protein (MBP); yeast protein substrates; synthetic peptide substrates, and polymer substrates. Of these, MBP and other standard protein substrates may be regarded as preferred. Other substrates may be identified, however, which are superior by way of affinity for the kinase, minimal perturbation of reaction kinetics, possession of single or homogenous reaction sites, ease of handling and post-reaction recover, potential for strong signal generation, and resistance or inertness to test compounds.

Measurement of the amount of substrate phosphorylated in the *ex vivo* assay of the invention may be carried out by means of immunoassay, radioassay or other well-known methods. In an immunoassay measurement, an antibody (such as a goat or mouse anti-phosphoserine/threonine antibody) may be used which is specific for phosphorylated moieties formed during the reaction. Using well-known ELISA techniques, the phosphoserine/threonine antibody complex would itself be detected by a further antibody linked to a label capable of developing a measurable signal (as for example a fluorescent or radioactive label). Additionally, ELISA-type assays in microtitre plates may be used to test purified substrates. Peraldi *et al.*, *J. Biochem.* 285: 71-78 (1992); Schraag *et al.*, *Anal. Biochem.* 211: 233-239 (1993); Cleavland, *Anal. Biochem.* 190: 249-253 (1990); Farley, *Anal. Biochem.* 203: 151-157 (1992) and Lozano, *Anal. Biochem.* 192: 257-261 (1991).

For example, detection schemes can measure substrate depletion during the kinase reaction. Initially, the phosphate source may be radiolabeled with an isotope such as  $^{32}\text{P}$  or  $^{33}\text{P}$ , and the amount of substrate phosphorylation may be measured by determining the amount of radiolabel incorporated into the substrate during the reaction. Detection may be accomplished by: (a) commercially available scintillant-containing plates and beads using a beta-counter, after adsorption to a filter or a microtitre well surface, or (b) photometric means after binding to a scintillation proximity assay bead or scintillant plate. Weernink and Kijken, *J. Biochem. Biophys. Methods* 31: 49, 1996; Braunwalder *et al.*, *Anal. Biochem.* 234: 23 (1996); Kentrup *et al.*, *J. Biol. Chem.* 271: 3488 (1996) and Rusken *et al.*, *Meth. Enzymol.* 200: 98 (1991).

Preferably, the substrate is attached to a solid support surface by means of non-specific or, preferably, specific binding. Such attachment permits separation of the phosphorylated substrate from unincorporated, labeled phosphate source (such as adenosine triphosphate prior to signal detection. In one embodiment, the substrate may be physically immobilized prior to reaction, as through the use of Nunc<sup>TM</sup> high protein binding plate (Hanke *et al.*, *J. Biol. Chem.* 271: 695 (1996)) or Wallac ScintiStrip<sup>TM</sup> plates (Braunwalder *et al.*, *Anal. Biochem.* 234: 23 (1996)). Substrate may also be immobilized after reaction by capture on, for example, P81 phosphocellulose (for basic peptides), PEI/acidic molybdate resin or DEAE, or TCA precipitation onto Whatman<sup>TM</sup> 3MM paper, Tiganis *et al.*, *Arch. Biochem. Biophys.* 325: 289 (1996); Morawetz *et al.*, *Mol. Gen. Genet.* 250: 17 (1996); Budde *et al.*, *Int J. Pharmacognosy* 33: 27 (1995) and Casnellie, *Meth. Enz.* 200: 115 (1991). Yet another possibility is the attachment of the substrate to the support surface, as by conjugation with



binding partners such as glutathione and streptavidin (in the case of GST and biotin), respectively) which have been attached to the support, or via antibodies specific for the tags which are likewise attached to the support.

Further detection methods may be developed which are preferred to those described above. Especially for use in connection with high-throughput screening, it is expected that such methods would exhibit good sensitivity and specificity, extended linear range, low background signal, minimal fluctuation, compatibility with other reagents, and compatibility with automated handling systems.

The *in vivo* efficacy of the treatment of the present invention can be studied against chemically induced tumors in various rodent models. Tumor cell lines propagated in *in vitro* cell cultures can be introduced in experimental rodents, *e.g.* mice by injection, for example by the subcutaneous route. Techniques for chemical inducement of tumors in experimental animals are well known in the art.

(b) *Biological detection techniques:*

The ability of the antagonist/agonist compounds of the invention to modulate the activity of *patched-2*, which itself modulates hedgehog signaling, may also be measured by scoring for morphological or functional changes associated with ligand binding. Any qualitative or quantitative technique known in the art may be applied for observing and measuring cellular processes which comes under the control of *patched-2*. The activity of the compounds of the invention can also be assessed in animals using experimental models of disorders caused by or related to dysfunctional *hedgehog* signaling. For example, ineffective *Dhh* hedgehog signaling in mice leads to viable but sterile mice. Additionally, proper *Shh* signaling is critical to murine embryonic development at the notochord and floor plate, neural tube, distal limb structures, spinal column and ribs. Improper *Shh* signaling, is also correlative with cyclopia. Any of these phenotypic properties could be evaluated and quantified in a screening assay for *patched-2* antagonists and/or agonist. Disease states associated with overexpression of hedgehog is associated with basal cell carcinoma while inactive *Shh* signaling leads to improper neural development.

The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosages for use in humans. The dosage of the compounds of the invention should lie within a range of circulating concentrations with little or no toxicity. The dosage may vary within this range depending on the dosage form employed and the route of administration.

(2) *Antisense oligonucleotides*

Another preferred class of antagonists involves the use of gene therapy techniques, include the administration of antisense oligonucleotides. Applicable gene therapy techniques include single or multiple administrations of therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. Reference short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by restricted uptake by the cell membrane, Zamecnik *et al.*, *Proc. Natl. Acad. Sci. USA*

83: 4143-4146 (1986). The anti-sense oligonucleotides can be modified to enhance their uptake, *e.g.*, by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques known for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, *ex vivo*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, *etc.* The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection, Dzau *et al.*, *Trends Biotech.* 11: 205-210 (1993). In some situations it is desirable to provide the nucleic acid source with an agent that targets the cells, such as an antibody specific for a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, *e.g.*, capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, and proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, *J. Biol. Chem.* 262: 4429-4432 (1987); Wagner *et al.*, *Proc. Natl. Acad. Sci. USA* 87: 3410-3414 (1990). For a review of known gene targeting and gene therapy protocols, see Anderson *et al.*, *Science* 256: 808-813 (1992).

In one embodiment of the invention, *patched-2* expression may be reduced by providing *patched-2*-expressing cells with an amount of *patched-2* antisense RNA or DNA effective to reduce expression of the *patched-2* protein.

## I. Diagnostic Uses

Another use of the compounds of the invention (*e.g.*, *patched-2*, *patched-2* variant and anti-*patched-2* antibodies) described herein is to help diagnose whether a disorder is driven, to some extent, by *patched-2* or hedgehog signaling. For example, basal cell carcinoma cells are associated with active *hedgehog* signaling, spermatocyte formation is associated with *Dhh* signaling, and defective *Ptch* and *Ptch-2* suppression may be associated with testicular carcinomas.

A diagnostic assay to determine whether a particular disorder is driven by *Ptch-2* modulated *hedgehog* signaling, can be carried out using the following steps: (1) culturing test cells or tissues; (2) administering a compound which can prevent *Ptch-2* (SEQ ID NO:2) binding with *Smo* (SEQ ID NO:17), thereby activating the *Hh* signaling pathway; and (3) measuring the amount of *Hh* signaling. The steps can be carried out using standard techniques in light of the present disclosure. For example, standard techniques can be used to isolate cells or tissues and culturing or *in vivo*.

Compounds of varying degree of selectivity are useful for diagnosing the role of *patched-2*. For example, compounds which inhibit *patched-2* in addition to another form of kinase can be used as an initial test compound to determine if one of several signaling ligands drive the disorder. The selective compounds can then be used to further eliminate the possible role of the other ligands in driving the disorder. Test compounds

should be more potent in inhibiting ligand-*patched-2* binding activity than in exerting a cytotoxic effect (*e.g.*, an  $IC_{50}/LD_{50}$  of greater than one). The  $IC_{50}$  and  $LD_{50}$  can be measured by standard techniques, such as an MTT assay, or by measuring the amount of LDH released. The degree of  $IC_{50}/LD_{50}$  of a compound should be taken into account in evaluating the diagnostic assay. For example, the larger the  $IC_{50}/LD_{50}$  ratio the more relative the information. Appropriate controls take into account the possible cytotoxic effect of a compound of a compound, such as treating cells not associated with a cell proliferative disorder (*e.g.*, control cells) with a test compound, can also be used as part of the diagnostic assay. The diagnostic methods of the invention involve the screening for agents that modulate the effects of *patched-2* upon *hedgehog* signaling. Exemplary detection techniques include radioactive labeling and immunoprecipitating (U.S.P. 5,385,915).

#### J. Pharmaceutical Compositions and Dosages

Therapeutic formulations of the compositions of the invention are prepared for storage as lyophilized formulations or aqueous solutions by mixing the *patched-2* molecule, agonist and/or antagonist having the desired degree of purity with optional "pharmaceutically-acceptable" or "physiologically-acceptable" carriers, excipients or stabilizers typically employed in the art (all of which are termed "excipients"). For example, buffering agents, stabilizing agents, preservatives, isotonicifiers, non-ionic detergents, antioxidants and other miscellaneous additives. (See Remington's Pharmaceutical Sciences, 16<sup>th</sup> Ed., A. Osol, Ed. (1980)). Such additives must be nontoxic to the recipients at the dosages and concentrations employed.

Buffering agents help to maintain the pH in the range which approximates physiological conditions. They are preferably present at concentration ranging from about 2mM to about 50 mM. Suitable buffering agents for use with the present invention include both organic and inorganic acids and salts thereof such as citrate buffers (*e.g.*, monosodium citrate-disodium citrate mixture, citric acid-trisodium citrate mixture, citric acid-monosodium citrate mixture, *etc.*), succinate buffers (*e.g.*, succinic acid-monosodium succinate mixture, succinic acid-sodium hydroxide mixture, succinic acid-disodium succinate mixture, *etc.*), tartrate buffers (*e.g.*, tartaric acid-sodium tartrate mixture, tartaric acid-potassium tartrate mixture, tartaric acid-sodium hydroxide mixture, *etc.*), fumarate buffers (*e.g.*, fumaric acid-monosodium fumarate mixture, *etc.*), fumarate buffers (*e.g.*, fumaric acid-monosodium fumarate mixture, fumaric acid-disodium fumarate mixture, monosodium fumarate-disodium fumarate mixture, *etc.*), gluconate buffers (*e.g.*, gluconic acid-sodium glyconate mixture, gluconic acid-sodium hydroxide mixture, gluconic acid-potassium glyconate mixture, *etc.*), oxalate buffer (*e.g.*, oxalic acid-sodium oxalate mixture, oxalic acid-sodium hydroxide mixture, oxalic acid-potassium oxalate mixture, *etc.*), lactate buffers (*e.g.*, lactic acid-sodium lactate mixture, lactic acid-sodium hydroxide mixture, lactic acid-potassium lactate mixture, *etc.*) and acetate buffers (*e.g.*, acetic acid-sodium acetate mixture, acetic acid-sodium hydroxide mixture, *etc.*). Additionally, there may be mentioned phosphate buffers, histidine buffers and trimethylamine salts such as Tris.

Preservatives are added to retard microbial growth, and are added in amounts ranging from 0.2% - 1% (w/v). Suitable preservatives for use with the present invention include phenol, benzyl alcohol, *meta*-cresol,

methyl paraben, propyl paraben, octadecyldimethylbenzyl ammonium chloride, benzalconium halides (*e.g.*, chloride, bromide, iodide), hexamethonium chloride, alkyl parabens such as methyl or propyl paraben, catechol, resorcinol, cyclohexanol, and 3-pentanol.

Isotonifiers sometimes known as "stabilizers" are present to ensure isotonicity of liquid compositions of the present invention and include polyhydric sugar alcohols, preferably trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol. Polyhydric alcohols can be present in an amount between 0.1% to 25% by weight, preferably 1% to 5% taking into account the relative amounts of the other ingredients.

Stabilizers refer to a broad category of excipients which can range in function from a bulking agent to an additive which solubilizes the therapeutic agent or helps to prevent denaturation or adherence to the container wall. Typical stabilizers can be polyhydric sugar alcohols (enumerated above); amino acids such as arginine, lysine, glycine, glutamine, asparagine, histidine, alanine, ornithine, L-leucine, 2-phenylalanine, glutamic acid, threonine, *etc.*, organic sugars or sugar alcohols, such as lactose, trehalose, stachyose, mannitol, sorbitol, xylitol, ribitol, myoinisitol, galactitol, glycerol and the like, including cyclitols such as inositol; polyethylene glycol; amino acid polymers; sulfur containing reducing agents, such as urea, glutathione, thiocitic acid, sodium thioglycolate, thioglycerol,  $\alpha$ -monothioglycerol and sodium thio sulfate; low molecular weight polypeptides (*i.e.* < 10 residues); proteins such as human serum albumin, bovine serum albumin, gelatin or immunoglobulins; hydrophilic polymers, such as polyvinylpyrrolidone monosaccharides, such as xylose, mannose, fructose, glucose; disaccharides such as lactose, maltose, sucrose and trisaccacharides such as raffinose; polysaccharides such as dextran. Stabilizers can be present in the range from 0.1 to 10,000 weights per part of weight active protein.

Non-ionic surfactants or detergents (also known as "wetting agents") are present to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stressed without causing denaturation of the protein.

Suitable non-ionic surfactants include polysorbates (20, 80, *etc.*), polyoxamers (184, 188 *etc.*), Pluronic® polyols, polyoxyethylene sorbitan monoethers (Tween®-20, Tween®-80, *etc.*). Non-ionic surfactants are present in a range of about 0.05 mg/ml to about 1.0 mg/ml, preferably about 0.07 mg/ml to about 0.2 mg/ml.

Additional miscellaneous excipients include bulking agents, (*e.g.* starch), chelating agents (*e.g.* EDTA), antioxidants (*e.g.*, ascorbic acid, methionine, vitamin E), and cosolvents.

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, it may be desirable to further provide an immunosuppressive agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsule prepared, for example, by coascervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacrylate) microcapsule, respectively, in colloidal drug delivery systems (for example,

liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences*, 16th edition, A. Osal, Ed. (1980).

The formulations to be used for in vivo administration must be sterile. This is readily accomplished, for example, by filtration through sterile filtration membranes.

5 Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the compounds of the invention, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No.3,773,919), copolymers of L-glutamic acid and ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™  
10 (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated compounds of the invention remain in the body for a long time, they may denature or aggregate as  
15 a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix  
20 compositions.

The amount of therapeutic polypeptide, antibody or fragment thereof which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to determine the dose-response curve and the pharmaceutical compositions of the invention first *in vitro*, and then in useful animal model systems  
25 prior to testing in humans. However, based on common knowledge of the art, a pharmaceutical composition effective in modulating *Dhh* and *Hh* signaling may provide a local *patched-2* protein concentration of between about 10 and 1000 ng/ml, preferably between 100 and 800 ng/ml and most preferably between about 200 ng/ml and 600 ng/ml of *Ptch-2* (SEQ ID NO:2).

In a preferred embodiment, an aqueous solution of therapeutic polypeptide, antibody or fragment  
30 thereof is administered by subcutaneous injection. Each dose may range from about 0.5 µg to about 50 µg per kilogram of body weight, or more preferably, from about 3 µg to about 30 µg per kilogram body weight.

The dosing schedule for subcutaneous administration may vary from once a week to daily depending on a number of clinical factors, including the type of disease, severity of disease, and the subject's sensitivity to the therapeutic agent.

*Patched-2* polypeptide may comprise an amino acid sequence or subsequence thereof as indicated in Fig. 1 (SEQ ID NO:2), active amino acid sequence derived therefrom, or functionally equivalent sequence as this subsequence is believed to comprise the functional portion of the *patched-2* polypeptide.

If the subject manifests undesired side effects such as temperature elevation, cold or flu-like symptoms, fatigue, etc., it may be desirable to administer a lower dose at more frequent intervals. One or more additional drugs may be administered in combination with *patched-2* to alleviate such undesired side effects, for example, an anti-pyretic, anti-inflammatory or analgesic agent.

\*\*\*\*\*

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

#### EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Rockville, Maryland.

#### EXAMPLE 1

##### Introduction:

At the cell surface, *Hh* function appears to be mediated by a multicomponent receptor complex involving *Ptch* (SEQ ID NO:4) and *Smo* (SEQ ID NO:17), two multi-transmembrane proteins initially identified as segment polarity genes in *Drosophila* and later characterized in vertebrates. Nakano, Y. *et al.*, *Nature* 341: 508-513 (1989); Goodrich *et al.*, *Gene Dev.* 10: 301-312 (1996); Marigo *et al.*, *Develop.* 122: 1225-1233 (1996); van den Heuvel *et al.*, *Nature* 382: 547-551 (1996); Alcedo *et al.*, *Cell* 86: 221-232 (1996); Stone *et al.*, *Nature* 384: 129-34 (1996). Both genetic and biochemical evidence support the existence of a receptor complex where *Ptch* (SEQ ID NO:4) is the ligand binding subunit, and where *Smo* (SEQ ID NO:17), a G-protein coupled receptor like molecule, is the signaling component. Stone *et al.*, *Nature* 384: 129-134 (1996), Marigo *et al.*, *Nature* 384: 176-79 (1996), Chen *et al.*, *Cell* 87: 553-63 (1996). Upon binding of *Hh* to *Ptch* (SEQ ID NO:4), the normal inhibitory effect of *Ptch* (SEQ ID NO:4) on *Smo* (SEQ ID NO:17) is relieved, allowing *Smo* (SEQ ID NO:17) to transduce the *Hh* signal across the plasma membrane.

**Results:**

It remains to be established if the *patched-Smoothed* receptor complex mediates the action of all 3 mammalian Hhs or if specific components exist. Recently, a second murine *patched* gene, *Ptch-2* (SEQ ID NO:7) was recently isolated [Motoyama *et al.*, *Nature Genet.* 18: 104-106 (1998)] but its function as a *Hh* receptor has not been established. In order to characterize *Ptch-2* (SEQ ID NO:2) and compare it to *Ptch* (SEQ ID NO:4) with respect to the biological function of the various *Hh* family members, we have screened EST databases with the *Ptch* (SEQ ID NO:4) protein and identified 2 EST candidates for a novel human *patched* gene. A full length cDNA encoding human *Ptch-2* (SEQ ID NO:2) was cloned from a testis library. The initiation ATG defines a 3612 nucleotide open reading frame encoding a 1204 amino acid long protein with a predicted molecular weight of approximately 131 kDa. The overall identity between human *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) is 54% (Fig. 1), while the identity between human *Ptch-2* (SEQ ID NO:2) and the recently described mouse *Ptch-2* (SEQ ID NO:7) is 90%. (Fig. 8). The most obvious structural difference between the two human *Ptch* proteins is a truncated C-terminal cytoplasmic domain in *Ptch-2* (SEQ ID NO:2). In addition, only one of the two glycosylation sites present in *Ptch* (SEQ ID NO:4) is conserved in *Ptch-2* (SEQ ID NO:2).

To determine if *Ptch-2* (SEQ ID NO:2) is a *Hh* receptor and if the two *patched* molecules are capable of discriminating between the various *Hh* ligands through specific binding, Applicants transfected human 293 embryonic kidney cells with *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) expression constructs and analyzed the cells for binding of *Shh*, *Dhh* and *Ihh* (SEQ ID NOS:14, 13, and 29, respectively). As shown on Figure 7A, binding of <sup>125</sup>I-*Shh* can be competed with an excess of *Shh*, *Dhh* or *Ihh* (SEQ ID NOS:14, 13, and 29, respectively). Scatchard analysis of the displacement curves indicates that all *Hhs* have similar affinity for *Ptch* (SEQ ID NO:4) (*Shh* (SEQ ID NO:14), 1.0nM; *Dhh* (SEQ ID NO:13), 2.6nM; *Ihh* (SEQ ID NO:29), 1.0nM) and *Ptch-2* (SEQ ID NO:2) (*Shh* (SEQ ID NO:14), 1.8nM; *Dhh* (SEQ ID NO:13), 0.6nM; *Ihh* (SEQ ID NO:29), 0.4nM) indicating that both *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) can serve as physiological receptors for the 3 mammalian *Hh* proteins.

Applicants next determined whether, like *Ptch* (SEQ ID NO:4), *Ptch-2* (SEQ ID NO:2) forms a physical complex with *Smo* (SEQ ID NO:17). Expression constructs for Flag-tagged *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) were transiently co-transfected in 293 cells with Myc-tagged *Smo* (SEQ ID NO:17). As described previously [Stone *et al.*, *Nature* 384: 129-34 (1996)], in cells expressing *Ptch* (SEQ ID NO:4) and *Smo* (SEQ ID NO:17), *Ptch* (SEQ ID NO:4) can be immunoprecipitated with antibodies against the epitope-tagged *Smo* (SEQ ID NO:15) (Fig. 7B). Similarly, *Ptch-2* (SEQ ID NO:2) can be immunoprecipitated with antibodies against the epitope-tagged *Smo* (SEQ ID NO:15) when the two proteins are co-expressed in 293 cells. Together, these results suggest a model where *Ptch-2* (SEQ ID NO:2) forms a multicomponent *Hh* receptor complex with *Smo* (SEQ ID NO:17) similar to the one described for *patched* (Stone *et al.*, *supra*). Interestingly, these results also demonstrate that the long C-terminal tail which is missing in *Ptch-2* (SEQ ID NO:2) is not required for the interaction with *Smo* (SEQ ID NO:17) as was already suggested by the analysis of

truncated *patched* (Stone *et al.*, *supra*). However, it remains possible that the absence of a C-terminal domain affects the capacity of *Ptch-2* (SEQ ID NO:2) to block signaling by *Smo* or leads to difference in signaling by *patched* compared to *patched-2*.

To further investigate whether *patched-2* could mediate the action of a specific Hh molecule based on its expression profile, Applicants have compared the expression pattern of *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2). First, Northern blot analysis using a probe specific for *Ptch-2* (SEQ ID NO:1) revealed high levels of *patched-2* mRNA in the testis (Fig. 4). By this method, *Ptch-2* (SEQ ID NO:1) expression was not detected in any other tissue analyzed including embryonic tissues (data not shown). This profile is very different from the one observed for *Ptch* (SEQ ID NO:18) which was not found in testis by Northern blot but in a large number of adult and embryonic tissues [Goodrich *et al.*, *Genes Dev.* 10: 301-312 (1996)]. More detailed analysis of the expression pattern of *Ptch* (SEQ ID NO:18) and *Ptch-2* (SEQ ID NO:1) was performed by *in situ* hybridization with particular attention to testis. As previously described (Motoyama *et al.*, *supra*), low levels of *Ptch-2* (SEQ ID NO:1) expression were detected in epithelial cells of the developing tooth and skin (data not shown). High levels of *Ptch-2* (SEQ ID NO:2) are expressed inside the seminiferous tubule, on the primary and secondary spermatocytes (Fig. 6B,6E) while only low levels of *Ptch* (SEQ ID NO:4) can be detected on the Leydig cells located in the interstitium of the seminiferous tubules (Fig. 6A). The primary and secondary spermatocytes are in close contact with the supporting Sertoli cells, the source of *Dhh* (SEQ ID NO:13) in the testis [Bitgood *et al.*, *Curr. Biol.* 6: 298-304 (1996)]. To determine which one of the 2 receptors is the most relevant mediator of *Dhh* (SEQ ID NO:13) activity in the testis, we have analyzed the expression profile of FuRK (SEQ ID NO:10), a Fused Related Kinase that was shown to be a component of the *Hh* signaling pathway (Zhang *et al.*, submitted; copending U.S.S.N. Serial Number 09/031,563, filed 26 Feb. 1998). Consistent with the idea that *Ptch-2* (SEQ ID NO:2) is the target of *Dhh* in the testis, we found that FuRK (SEQ ID NO:10) is expressed only in germ cells where it colocalizes with *Ptch-2* (SEQ ID NO: 2) (Figure 4c,f). *Dhh* (SEQ ID NO:13) is required for proper differentiation of germ cells since male *Dhh*-deficient mice are sterile due to lack of mature sperm (Bitgood *et al.*, *supra*). Our data suggest that *Dhh* (SEQ ID NO:13) acts directly on germ cells through *Ptch-2* (SEQ ID NO:2) while the function of *Ptch* (SEQ ID NO:4) expressed at low levels on testosterone producing Leydig cells is unclear.

#### Discussion:

Loss of heterozygosity (LOH) for *patched* was reported to occur with high frequency in familial as well as sporadic basal cell carcinoma [Johnson *et al.*, *Science* 272: 1668-71 (1996); Hahn *et al.*, *Cell* 85: 841-51 (1996); Gailani *et al.*, *Nature Genetics* 14: 78-81; Xie *et al.*, *Cancer Res.* 57: 2369-72 (1997)], suggesting that it functions as a tumor suppressor. According to the receptor model described above, loss of *patched* function may result in aberrant signaling by *Smo* (SEQ ID NO:17), leading to hyperproliferation of the skin basal cell layer. If, as suggested above, *patched-2* mediates the function of *Dhh*, loss of *Ptch-2* (SEQ ID NO:2) may lead



to tumor formation in tissues where *Smo* (SEQ ID NO:17) activity is controlled by *patched-2*. The gene encoding *patched-2* was mapped by fluorescence *in situ* hybridization and by PCR using a radiation hybrid panel to human chromosome 1p33-34 (data not shown). Interestingly, recent analysis of recurrent chromosomal abnormalities in testicular tumors, including seminomas, revealed a deletion of the region 1p32-36 [Summersgill *et al.*, *B. J. Cancer* 77: 305-313 (1998)]. Loss of this region encompassing the *patched-2* locus was consistent in 36% of the germ cell tumor cases. These data raise the possibility that, like *patched* in basal cell carcinoma and medulloblastoma, *patched-2* may be a tumor suppressor in *Dhh* (SEQ ID NO:13) target cells such as spermatocytes, further implicating *Hh* signaling in cancer.

In summary, our data demonstrate that both *patched* and *patched-2* are genuine *Hh* receptors and that they are both capable of forming a complex with *Smo* (SEQ ID NO:17). Although binding data indicate that *patched* and *patched-2* do not discriminate between the various *Hh* ligands through affinity differences, the distinct tissue distribution of these 2 receptors suggests that *in vivo*, *patched* may be the primary receptor for *Shh* whereas *Ptc-2* will mediate mainly *Dhh* signaling. The function of *patched* expression in Leydig cells in the absence of some of the *Hh* signaling components remain to be explained. Similarly, it will be of interest to determine if *patched-2* plays a role when expressed in *Shh* expressing cells present in the developing tooth and skin Motoyama *et al.*, *Nature Genet.* 18: 104-106 (1998). Finally, the existence of *patched-2* raises the question of whether additional *patched* receptors exist, in particular one that mediates the function of *Ihh* (SEQ ID NO:29).

## Material and Methods:

### 1. Isolation of human *patched-2* cDNA clones

An expressed sequence tag (EST) DNA database (LIFESEQ®, Incyte Pharmaceuticals, Palo Alto, CA) was searched for a human homologue of the *Drosophila* segment polarity gene *patched-2*. Two ESTs (Incyte #905531 and 1326258) (Fig. 2) (SEQ ID NOS: 3 and 5, respectively) were identified as a potential candidates. In order to identify human cDNA libraries containing human *patched-2* clones, human cDNA libraries in pRK5 were first screened by PCR using the following primers:

5'-905531(A): 5'-AGGCGGGGGATCACAGCA-3' (SEQ ID NO:19)

3'-905531(A): 5'-ATACCAAAGAGTTCCACT-3' (SEQ ID NO:20)

A fetal lung library was selected and enriched for *patched-2* cDNA clones by extension of single stranded DNA from plasmid libraries grown in dut<sup>-</sup>/ung<sup>-</sup> host using the 3'-905531(A) primer in a reaction containing 10μl of 10x PCR Buffer (Klentaq®), 1μl dNTP (200 μM), 1 μl library DNA (200 ng), 0.5 μl primer, 86.5 μl H<sub>2</sub>O and 1 μl of Klentaq® (Clontech) added after a hot start. The reaction was denatured for 1 min. at 95°C, annealed for 1 min. at 60°C then extended for 20 min. at 72°C. DNA was extracted with phenol/CHCl<sub>3</sub>, ethanol precipitated,

then transformed by electroporation into DH10B (Gibco/BRL) host bacteria. Colonies from each transformation were replica plated on nylon membranes and screened with an overlapping oligo probe derived from the EST sequence (#905531) of the following sequence:

5'-*Ptch2* probe: 5'-CTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGC-3' (SEQ ID NO:21)

3'-*Ptch2* probe: 5'-AGAGCACAGACGAGGAAAGTGCACACCAGCAGGATGCAGACGGCC-3' (SEQ ID NO:22)

The oligo probe was labeled with [ $\gamma$ -<sup>32</sup>P]-ATP and T4 polynucleotide kinase. Filters were hybridized overnight at 42°C in 50% formamide, 5xSSC, 10xDenhardt's, 0.05M sodium phosphate (pH 6.5), 0.1% sodium pyrophosphate, 50 µg/ml of sonicated salmon sperm DNA. The filters were then rinsed in 2x SSC and washed in 0.1x SSC, 0.1% SDS then exposed to Kodak® X Ray films.

Using this procedure, a partial clone was isolated from the fetal brain library (clone 3A – Fig. 10) (SEQ ID NO:8). In order to isolate the missing 5'-sequence, a testis library (see northern blot analysis, infra) was screened. The primer set used to amplify a 204 bp probe from clone 3A to probe the testis library was:

RACE 5: 5'-ACTCCTGACTTGTAGCAGATT-3' (SEQ ID NO:23) and

RACE 6: 5'-AGGCTGCATACACCTCTCAGA-3'. (SEQ ID NO:24)

The amplified probe was purified by excision from an agarose gel and labeled with a random primer labeling kit (Boehringer Mannheim). Several clones were isolated, including one (clone 16.1 – Fig. 11 (SEQ ID NO:9)) containing a potential initiation methionine. A full length cDNA encoding *patched-2* was reconstructed by assembling several of these clones. The full length cDNA encoding human *Ptch-2* (Fig. 1) (SEQ ID NO:1) has a 3612 nucleotide long open reading frame encoding a 1204 amino acid protein with a 144 kDa predicted molecular weight. Alignment with human *Ptch* (SEQ ID NO:4) reveals a 53% identity between the 2 molecules at the amino acid level (Fig. 3). All 12 transmembrane domains are conserved. The most significant difference is a shorter C-terminal intracellular domain in *Ptch-2* (SEQ ID NO:2) compared to *Ptch* (SEQ ID NO:4).

## 2. Northern blot analysis:

In order to determine the best tissue source for isolation of the complete full length *Ptch-2* cDNA as well as to determine its expression profile, we probed human multiple tissue northern blots (Clontech) with a 752 bp fragment amplified from the 3' untranslated region of *Ptch-2* (SEQ ID NO:2) using the following primers:

TM2: TM2 5-GCTTAGGCCCGAGGAGAT-3' (SEQ ID NO:25)

UTR2: 5'-AACTCACAACCTTTCTCTCCA-3'. (SEQ ID NO:26)

The resulting fragment was gel purified and labeled by random priming. The blots were hybridized in ExpressHyb® hybridization solution (Clontech) in the presence of 1 x 10<sup>6</sup> cpm/ml <sup>32</sup>P-labeled probe at 42°C overnight. The blots were washed in 2x SSC at room temperature for 10 minutes and washed in 0.1 x SSC/0.1

% SDS at 42°C for 30 minutes then exposed to x-ray film overnight. Fig. 4 shows that *Ptch-2* message is expressed at high levels in only the testis.

### 3. Chromosomal localization:

The primers TM2 (SEQ ID NO:25) and UTR2 (SEQ ID NO:26) described above were used to screen the Genome Systems (St. Louis ,MO) BAC library. Two individual BAC clones were obtained from this library and chromosomal localization of both of the clones by FISH indicated that *Ptch-2* (SEQ ID NO:2) maps to human chromosome 1p33-34 (FIG 5). Loss of heterozyosity (LOH) for *patched* was reported to occur with high frequency in basal cell carcinoma . Loss of *patched* function is thought to lead to constitutive signaling by *Smoothed* (*Smo* (SEQ ID NO:17)), resulting in hyperproliferation of the basal layer of the dermis. A similar mechanism may lead to the formation of germ cell tumors. This model proposes that the first step in the progression of a germ cell tumor is an initial loss of DNA by a germ cell precursor, leading to a neoplastic germ cell which then forms a seminoma [De Jong *et al.*, *Cancer Genet. Cytogenet.* 48: 143-167 (1990)]. From the invasive seminoma, all other forms of germ cell tumor types develop. Approximately 80% of all germ cell tumors correlate with an isochromosome 12p (i12p) and is found at a higher frequency in non-seminomas than seminomas [Rodriguez *et al.*, *Cancer Res* 52: 2285-2291 (1992)]. However, analysis of recurrent chromosomal abnormalities in testicular tumors including seminomas revealed a deletion of the region 1p32-36. Loss of this region was consistent in 36% of the germ cell tumor cases of in a recent study Summersgill *et al.*, *B. J. Cancer* 57: 305-313 (1998)]. A similar deletion of chromosome 1p32-36 has been reported at a frequency of 28% in oligodendrogliomas Bello, *et al.*, *Int. J. Cancer* 57: 172-175 (1994). While expression of *patched-2* (SEQ ID NO:2) in the brain was not examined here in detail, *patched-2* (SEQ ID NO:2) is thought to be the *Dhh* receptor (see below) and expression of *Dhh* by murine Schwann cells was previously reported [Bitgood *et al.*, *Develop. Biol.* 172: 126-138 (1995)]. Since *patched-2* (SEQ ID NO:2) localizes to chromosome 1p33-34 it is possible that *patched-2* regulates *Smo* (SEQ ID NO:17) signaling in *Dhh* target cells and that loss of *patched-2* function leads to abnormal *Smo* (SEQ ID NO:17) signaling in these cells and subsequent tumor formation.

### 4. In situ hybridization:

Mouse testis sections were cut at 16  $\mu$ m, and processed for in situ hybridization by the method described in Phillips *et al.*, *Science* 250: 290-294 (1990). <sup>33</sup>P-UTP labeled RNA probes were generated as described in Melton *et al.*, *Nucleic Acids Res.* 12: 7035-7052 (1984). Sense and antisense probes were synthesized from the 3' non coding region of the mouse *Ptch* or *Ptch-2* and from a mouse FuRK cDNA fragment corresponding to the region encoding amino acid 317-486 of the human sequence using T3 and T7, respectively.

*Ptch*:

**503 (Anti-sense)**

5'GGATTCTAATACGACTCACTATAGGGCCCAATGGCCTAAACCGACTGC3' (SEQ ID NO:27)

**503 (Sense)**

5 'CTATGAAATTAACCCTCACTAAAGGGACCCACGGCCTCTCCTCACA3' (SEQ ID NO:28)

*Ptch2*:

**504 (Anti-sense)**

5'GGATTCTAATACGACTCACTATAGGGCCCTAAACTCCGCTGCTCCAC3' (SEQ ID NO:12)

**504 (Sense)**

10 5'CTATGAAATTAACCCTCACTAAAGGGAGCTCCCGTGAGTCCCTATGTG3' (SEQ ID NO:11)

FuRK sense and antisense were synthesized from a mouse *fused* DNA fragment using T3 and T7, respectively, corresponding to the region encoding amino acid residues 317-486 of the human sequence (Zhang *et al.*, submitted, 1998; copending U.S.S.N. 09/031,563, filed 26 Feb. 1998).

15 Figure 6 illustrates that, although both *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) are expressed in testis, their expression pattern does not overlap. *Ptch* (SEQ ID NO:4) is expressed in the Leydig cells of the interstitium while *Ptch-2* (SEQ ID NO:2) is expressed in the primary and secondary spermatocytes.

The expression of *Ptch-2* (SEQ ID NO:2) specifically in the developing spermatogonia suggest that *Ptch-2* (SEQ ID NO:2) is the immediate target of *Dhh* (SEQ ID NO:13). *Dhh* (SEQ ID NO:13) is expressed by Sertoli cells and mice deficient in *Dhh* (SEQ ID NO:13) are sterile because of a defect in sperm production [Bitgood *et al.*, *Curr. Biol.* 6: 298-304 (1996)]. Although this effect on germ cells was thought to be indirect and mediated by *Ptch* present on Leydig cells, our data suggest that *Dhh* directly acts on germ cells through *Ptch-2*.

This is further demonstrated by the localization of FuRK (SEQ ID NO:10), an intracellular kinase homologous to *Drosophila Fused* and involved in transducing the Hedgehog (*Hh*) signal. As shown in Figure 6, FuRK (SEQ ID NO:10) is colocalizes with *Ptch-2* (SEQ ID NO:2) in germ cells and not with *Ptch* (SEQ ID NO:4) in Leydig cells, suggesting that *Ptch-2* and not *Ptch* will be able to transduce the *Dhh* signal. These results suggest that *Ptch-2* is a *Dhh* receptor.

*Ptch-2* mRNA levels in *Smo-M2* (SEQ ID NO:16) transgenic mice [A *Smo* mutation which results in autonomous phenotypes similar to BCC, Xie *et al.*, *Nature* 391: 90-92 (1998)] can be increased upon abnormal activation of the *Hh* signaling pathway. As indicated in Fig. 9, patch-2 levels were high in tumor cells (although lower than *Ptch* levels). This suggests that antibodies directed toward *Ptch-2* may be useful in the treatments of BCC.

5. *Immunoprecipitation with Smo:*

The binding of *Ptch-2* to *Smo* (SEQ ID NO:17) was assessed by cotransfection using a transient transfection system of a myc-epitope tagged *Smo* (SEQ ID NO:15) and a FLAG-epitope tagged *Ptch* or *Ptch2* expression construct in 293 cells using standard techniques (Gorman, C., *DNA Cloning: A Practical Approach*, Clover, DM ed., Vol. 11, pp. 143-190, IRL Press, Washington, D.C.). 36 hours after transfection, the cells were lysed in 1% NP-40 and immunoprecipitated overnight with the 9E10 anti-myc antibody or with the M2 anti-FLAG antibody (IBI-Kodak) followed by protein A Sepharose, and then separated on a denatured 6% polyacrylamide gel. Proteins were detected by transfer to nitrocellulose and probing with antibodies to Flag or Myc epitopes, using the ECL detection system (Amersham). Figure 7B indicates that both *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) are expressed at the same level (IP Flag, Blot Flag) and that like *Ptch* (SEQ ID NO:4), *Ptch-2* (SEQ ID NO:2) forms a physical complex with *Smo* (SEQ ID NO:17). These results suggest that like *patched*, *patched-2* controls *Hh* signaling through its interaction with *Smo* (SEQ ID NO:17).

6. *Hh Binding:*

To determine whether *Ptch-2* is able to bind to the various hedgehog ligands, 293 cells were transfected with *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) using standard procedures. Cells were incubated with 100 pM <sup>125</sup>I-*Shh* (19kD amino terminal fragment of murine *Shh* (SEQ ID NO:14)) in the presence or absence of excess unlabeled *Shh* (SEQ ID NO:14) or *Dhh* (SEQ ID NO:13) for 2h at room temperature. After equilibrium was reached, the ligand bound cells were centrifuged through a continuous sucrose gradient to separate unincorporated and then counted in a scintillation counter. Figure 7A shows that both *Dhh* (SEQ ID NO:13) and *Shh* (SEQ ID NO:14) bind to *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2). Varying concentrations of cold competitor indicate that the 2 ligands have similar affinity for *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2).

Example 2

Expression of *patched-2* in *E. coli*

The DNA sequence encoding human *patched-2* is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites that correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar *et al.*, *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences that encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the vertebrate *patched-2* coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized vertebrate *patched-2* protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

### Example 3

#### Expression of patched-2 in mammalian cells

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the vertebrate *patched-2* DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the vertebrate *patched-2* DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-*patched-2*.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-*patched-2* DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl<sub>2</sub>. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO<sub>4</sub>, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml <sup>35</sup>S-cysteine and 200 µCi/ml <sup>35</sup>S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of vertebrate *patched-2* polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, vertebrate *patched-2* may be introduced into 293 cells transiently using the dextran sulfate method described by Sompariyac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-*patched-2* DNA is added. The cells are first

concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed vertebrate *patched-2* can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, vertebrate *patched-2* can be expressed in CHO cells. The pSVi-*patched-2* can be transfected into CHO cells using known reagents such as CaPO<sub>4</sub> or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as <sup>35</sup>S-methionine. After determining the presence of vertebrate *patched-2* polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed vertebrate *patched-2* can then be concentrated and purified by any selected method.

Epitope-tagged vertebrate *patched-2* may also be expressed in host CHO cells. The vertebrate *patched-2* may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into an expression vector. The poly-his tagged vertebrate *patched-2* insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged vertebrate *patched-2* can then be concentrated and purified by any selected method, such as by Ni<sup>2+</sup>-chelate affinity chromatography.

#### Example 4

##### Expression of vertebrate *patched-2* in Yeast

The following method describes recombinant expression of vertebrate *patched-2* in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of vertebrate *patched-2* from the ADH2/GAPDH promoter. DNA encoding vertebrate *patched-2*, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of vertebrate *patched-2*. For secretion, DNA encoding vertebrate *patched-2* can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of vertebrate *patched-2*.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant vertebrate *patched-2* can subsequently be isolated and purified by removing the yeast

cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing vertebrate *patched-2* may further be purified using selected column chromatography resins.

5

## Example 5

Expression of vertebrate *patched-2* in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of vertebrate *patched-2* in Baculovirus-infected insect cells.

The vertebrate *patched-2* is *patched-2* upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the vertebrate *patched-2* or the desired portion of the vertebrate *patched-2* (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley *et al.*, Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged vertebrate *patched-2* can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert *et al.*, *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A<sub>280</sub> baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni<sup>2+</sup>-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged vertebrate *patched-2* are pooled and dialyzed against loading buffer.



Alternatively, purification of the IgG tagged (or Fc tagged) vertebrate *patched-2* can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

#### Example 6

##### Preparation of Antibodies that Bind Vertebrate *patched-2*

This example illustrates preparation of monoclonal antibodies, which can specifically bind vertebrate *patched-2*.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified vertebrate *patched-2*, fusion proteins containing vertebrate *patched-2*, and cells expressing recombinant vertebrate *patched-2* on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the vertebrate *patched-2* immunogen (E.g., extracellular portions or cells expressed *Ptch-2*) emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect vertebrate *patched-2* antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of vertebrate *patched-2*. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then patched-2 (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-patched-2 cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against vertebrate *patched-2*. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against vertebrate *patched-2* is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti- vertebrate *patched-2* monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

## Example 7

Gli Luciferase Assay

5 The following assay may be used to measure the activation of the transcription factor *GLI*, the mammalian homologue of the *Drosophila cubitus interruptus* (Ci). It has been shown that *GLI* is a transcription factor activated upon *SHh* stimulation of cells.

10 Nine (9) copies of a GLI binding site present in the HNF3 $\beta$  enhancer, (Sasaki *et al.*, *Development* 124: 1313-1322 (1997)), are introduced in front of a thymidine kinase minimal promoter driving the luciferase reporter gene in the pGL3 plasmid (Promega). The sequence of the *GLI* binding sequence is: TCGACAAGCAGGGAACACCCAAGTAGAAGCTC (p9XGLiLuc) (SEQ ID NO:31), while the negative control sequence is: TCGACAAGCAGGGAAGTGGGAAGTAGAAGCTC (p9XmGLiLuc) (SEQ ID NO:32). These constructs are cotransfected with the full length *Ptch*-2 and *Smo* in C3H10T1/2 cells grown in F12, DMEM (50:50), 10% FCS heat inactivated. The day before transfection 1 x 10<sup>5</sup> cells per well was inoculated in 15 6 well plates, in 2 ml of media. The following day, 1  $\mu$ g of each construct is cotransfected in duplicate with 0.025 mg ptkRenilla luciferase plasmid using lipofectamine (Gibco-BRL) in 100  $\mu$ l OptiMem (with GlutaMAX) as per manufacturer's instructions for 3 hours at 37°C. Serum (20%, 1 ml) is then added to each well and the cells were incubated for 3 more hours at 37°C. Cells are then washed twice with PBS, then incubated for 48 hours at 37°C in 2 ml of media. Each well is then washed with PBS, and the cells lysed in 0.5 20 ml Passive Lysis Buffer (Promega) for 15 min. at room temperature on a shaker. The lysate is transferred in eppendorf tubes on ice, spun in a refrigerated centrifuge for 30 seconds and the supernatant saved on ice. For each measure, 20  $\mu$ l of cell lysate is added to 100  $\mu$ l of LARII (luciferase assay reagent, Promega) in a polypropylene tube and the luciferase light activity measured. The reaction is stopped by the addition of Stop and Glow buffer (Promega), mixed by pipetting up and down 3 to 5 times and *Renilla* luciferase lights activity 25 is measured on the luminometer.

\* \* \* \*

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

5	<u>Designation:</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	pRK7.hptc2.Flag-1405	209778	4/14/98

10 This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

20 The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

25 The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

## Sequence Listing

<110> de Sauvage, Frederic  
Carpenter, David A.

5

<120> Patched-2

<130> P1405R1

10

<141> 1999-04-14

<150> US 60/081,884

<151> 1998-04-15

15

<160> 32

<210> 1

<211> 4030

<212> DNA

20

<213> Homo sapiens

<400> 1

gttattttcag gccatggtgt tgcgcgaat taattcccga tccagacatg 50

25

ataagataca ttgatgagtt tggacaaacc acaactagaa tgcagtgaaa 100

aaaatgcttt atttgtgaaa tttgtgatgc tattgcttta tttgtaacca 150

30

ttataagctg caataaaciaa gttggggccat ggcgccaag cttctgcagg 200

tcgactctag aggatccccg ggaattccg gcatgactcg atcgccgcc 250

ctcagagagc tgcccccgag ttacacaccc ccagctcgaa ccgcagcacc 300

35

ccagatccta gctgggagcc tgaaggctcc actctggctt cgtgcttact 350

tccagggcct gctcttctct ctgggatgcg ggatccagag acattgtggc 400

40

aaagtgtctt ttctgggact gttggccttt ggggccctgg cattaggtct 450

ccgcatggcc attattgaga caaacttgga acagctctgg gtagaagtgg 500

gcagccgggt gagccaggag ctgcattaca ccaaggagaa gctgggggag 550

45

gaggctgcat acacctctca gatgctgata cagaccgcac gccaggaggg 600

agagaacatc ctcacacccg aagcacttg cctccacctc caggcagccc 650

50

tcactgccag taaagtccaa gtatcactct atgggaagtc ctgggatttg 700

aacaaaatct gctacaagtc aggagttccc cttattgaaa atggaatgat 750

tgagtggatg attgagaagc tgtttccgtg cgtgatectc acccccctcg 800

55

actgcttctg ggagggagcc aaactccaag ggggctccgc ctacctgcc 850

ggccgcccg ataccagtg gaccaacctg gatccagagc agctgctgga 900

60

ggagctgggt ccctttgcct cccttgaggg cttccgggag ctgctagaca 950

aggcacaggt gggccaggcc tacgtggggc ggccctgtct gcaccctgat 1000

039046-11001

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60

gacctccact gccacactag tgccccaac catcacagca ggcaggctcc 1050  
 caatgtggct cagcagctga gtgggggctg ccatggcttc tcccacaaat 1100  
 tcatgcactg gcaggaggaa ttgctgctgg gaggcattggc cagagacccc 1150  
 caaggagagc tgctgagggc agaggccctg cagagcacct tcttgctgat 1200  
 gagtccccgc cagctgtacg agcatttccg ggggtgactat cagacacatg 1250  
 acattggctg gagtgaggag caggccagca cagtgtctaca agcctggcag 1300  
 cggcgctttg tgcagctggc ccaggaggcc ctgcctgaga acgcttccca 1350  
 gcagatccat gccttctcct ccaccaccct ggatgacatc ctgcatgcgt 1400  
 tctctgaagt cagtgtctgc cgtgtggtgg gaggtatatc gctcatgctg 1450  
 gcctatgcct gtgtgaccat gctgcggtgg gactgcgcc agtcccaggg 1500  
 ttccgtgggc cttgcggggg tactgtggt ggccctggcg gtggcctcag 1550  
 gccttgggct ctgtgcctg ctggcatca ccttcaatgc tgccactacc 1600  
 cagggtctgc ctttcttggc tctgggaatc ggcgtggatg acgtattcct 1650  
 gctggcgcat gccttcacag aggtctctgc tggcaccct ctccaggagc 1700  
 gcatgggcga gtgtctgcag cgcacgggca ccagtgtcgt actcacatcc 1750  
 atcaacaaca tggcgcctt cctcatggt gccctcgttc ccatccctgc 1800  
 gctgcgagcc ttctccctac aggcggccat agtggttggc tgcaccttg 1850  
 tagccgtgat gcttgtcttc ccagccatcc tcagcctgga cctacggcgg 1900  
 cgccactgcc agcgccttga tgtgtctgc tgccttctca gtccctgctc 1950  
 tgctcagggtg attcagatcc tgccccagga gctgggggac gggacagtac 2000  
 cagtgggcat tgcccacctc actgccacag ttcaagcctt taccactgt 2050  
 gaagccagca gccagcatgt ggtcaccatc ctgcctccc aagcccacct 2100  
 ggtgccccca cttcttgacc cactgggctc tgagctcttc agccttgag 2150  
 ggtccacacg ggaccttcta ggccaggagg aggagacaag gcagaaggca 2200  
 gcctgcaagt ccctgcctg tgcccgtgg aatcttgccc atttgcctcg 2250  
 ctatcagttt gcccgcttgc tgcctcagtc acatgccaag gccatcgtgc 2300  
 tggtgctctt tggtgctctt ctgggctga gcctctacgg agccaccttg 2350  
 gtgcaagacg gcctggccct gacggatgtg gtgcctcggg gcaccaagga 2400  
 gcatgccttc ctgagcgccc agctcaggta cttctccctg tacgagggtg 2450  
 ccctggtgac ccagggtggc tttgactacg cccattccca acgcgcctc 2500

5 tttgatctgc accagcgctt cagttccctc aaggcgggtgc tgccccacc 2550  
 ggccacccag gcaccccgca cctggctgca ctattaccgc aactggctac 2600  
 10 aggggaatcca ggctgccttt gaccaggact gggcttctgg gcgcatcacc 2650  
 cgccactcgt accgcaatgg ctctgaggat ggggccttgg cctacaagct 2700  
 gctcatccag actggagacg cccaggagcc tctggatttc agccagctga 2750  
 15 ccacaaggaa gctggtggac agagagggac tgattccacc cgagctcttc 2800  
 tacatggggc tgaccgtgtg ggtgagcagt gaccccttgg gtctggcagc 2850  
 ctcacaggcc aacttctacc cccacctcc tgaatggctg cacgacaaat 2900  
 acgacaccac gggggagAAC ctctgcctcc cgccagctca gcccttggag 2950  
 20 tttgcccagt tccccttcc tctgcgtggc ctccagaaga ctgcagactt 3000  
 tgtggaggcc atcgaggggg cccgggcagc atgcgcagag gccggccagg 3050  
 ctgggggtgca cgcctacccc agcggctccc ctttctctt ctgggaacag 3100  
 25 tatctggggc tgcggcgtg ctctctgtg gccgtctgca tctgtctggt 3150  
 gtgcactttc ctctctgtg ctctgtctg cctcaacccc tggacggtg 3200  
 gcctcatagt gctggtcctg gcgatgatga cagtggaaact ctttggatat 3250  
 30 atgggtttcc tgggcatcaa gctgagtgcc atccccttgg tgatccttgt 3300  
 ggccctctgta ggcatggcg ttgagttcac agtccacgtg gctctgggct 3350  
 35 tcttgaccac ccagggcagc cggaacctgc gggccgcccA tgcccttgag 3400  
 cacacatttg ccccgctgac cgatggggcc atctccacat tgctgggtct 3450  
 gctcatgctt gctggttccc actttgactt cattgtaagg tacttctttg 3500  
 40 cggcgtgac agtgtcacg ctctggggc tctccatgg actcgtgctg 3550  
 ctgcctgtgc tgctgtccat cctgggcccg ccgccagagg tgatacagat 3600  
 45 gtacaaggaa agcccagaga tcttgagtcc accagctcca cagggaggcg 3650  
 ggcttaggtg gggggcatcc tctccctgc cccagagctt tgccagagtg 3700  
 actacctcca tgaccgtggc catccacca cccccctgc ctggtgccta 3750  
 50 catcatcca gccctgatg agcccccttg gtcccctgct gccactagct 3800  
 ctggcaacct cagttccagg ggaccaggtc cagccactgg gtgaaagagc 3850  
 55 agctgaagca cagagacat gtgtggggcg tgtggggtca ctgggaagca 3900  
 ctgggtctgg tgttagacgc aggacggacc cctggagggc cctgctgctg 3950  
 60 ctgcatcccc tctccgacc cagctgtcat gggcctccct gatatcgaat 4000  
 tcaatcgata gaaccgaggt gcagttggac 4030

<210> 2  
 <211> 1203  
 <212> PRT  
 5 <213> Homo sapiens

<400> 2

Met	Thr	Arg	Ser	Pro	Pro	Leu	Arg	Glu	Leu	Pro	Pro	Ser	Tyr	Thr
1				5					10					15
Pro	Pro	Ala	Arg	Thr	Ala	Ala	Pro	Gln	Ile	Leu	Ala	Gly	Ser	Leu
				20					25					30
Lys	Ala	Pro	Leu	Trp	Leu	Arg	Ala	Tyr	Phe	Gln	Gly	Leu	Leu	Phe
				35					40					45
Ser	Leu	Gly	Cys	Gly	Ile	Gln	Arg	His	Cys	Gly	Lys	Val	Leu	Phe
				50					55					60
Leu	Gly	Leu	Leu	Ala	Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Arg	Met
				65					70					75
Ala	Ile	Ile	Glu	Thr	Asn	Leu	Glu	Gln	Leu	Trp	Val	Glu	Val	Gly
				80					85					90
Ser	Arg	Val	Ser	Gln	Glu	Leu	His	Tyr	Thr	Lys	Glu	Lys	Leu	Gly
				95					100					105
Glu	Glu	Ala	Ala	Tyr	Thr	Ser	Gln	Met	Leu	Ile	Gln	Thr	Ala	Arg
				110					115					120
Gln	Glu	Gly	Glu	Asn	Ile	Leu	Thr	Pro	Glu	Ala	Leu	Gly	Leu	His
				125					130					135
Leu	Gln	Ala	Ala	Leu	Thr	Ala	Ser	Lys	Val	Gln	Val	Ser	Leu	Tyr
				140					145					150
Gly	Lys	Ser	Trp	Asp	Leu	Asn	Lys	Ile	Cys	Tyr	Lys	Ser	Gly	Val
				155					160					165
Pro	Leu	Ile	Glu	Asn	Gly	Met	Ile	Glu	Trp	Met	Ile	Glu	Lys	Leu
				170					175					180
Phe	Pro	Cys	Val	Ile	Leu	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly
				185					190					195
Ala	Lys	Leu	Gln	Gly	Gly	Ser	Ala	Tyr	Leu	Pro	Gly	Arg	Pro	Asp
				200					205					210
Ile	Gln	Trp	Thr	Asn	Leu	Asp	Pro	Glu	Gln	Leu	Leu	Glu	Glu	Leu
				215					220					225
Gly	Pro	Phe	Ala	Ser	Leu	Glu	Gly	Phe	Arg	Glu	Leu	Leu	Asp	Lys
				230					235					240
Ala	Gln	Val	Gly	Gln	Ala	Tyr	Val	Gly	Arg	Pro	Cys	Leu	His	Pro
				245					250					255
Asp	Asp	Leu	His	Cys	Pro	Pro	Ser	Ala	Pro	Asn	His	His	Ser	Arg
				260					265					270

5

10

15

20

25

30

35

40

45

Ser Gln Gly Ser Val Gly Leu Ala Gly Val Leu Leu Val Ala Leu  
425 430 435

Ala Val Ala Ser Gly Leu Gly Leu Cys Ala Leu Leu Gly Ile Thr  
440 445 450

Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly  
455 460 465

Ile Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Thr Glu  
470 475 480

Ala Leu Pro Gly Thr Pro Leu Gln Glu Arg Met Gly Glu Cys Leu  
485 490 495

Gln Arg Thr Gly Thr Ser Val Val Leu Thr Ser Ile Asn Asn Met  
500 505 510





5

10

15

20

25

30

35

40

45

Patent # 8,400,660

	Leu Ile Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly	995	1000	1005
5	Ile Met Gly Phe Leu Gly Ile Lys Leu Ser Ala Ile Pro Val Val	1010	1015	1020
	Ile Leu Val Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His	1025	1030	1035
10	Val Ala Leu Gly Phe Leu Thr Thr Gln Gly Ser Arg Asn Leu Arg	1040	1045	1050
	Ala Ala His Ala Leu Glu His Thr Phe Ala Pro Val Thr Asp Gly	1055	1060	1065
15	Ala Ile Ser Thr Leu Leu Gly Leu Leu Met Leu Ala Gly Ser His	1070	1075	1080
20	Phe Asp Phe Ile Val Arg Tyr Phe Phe Ala Ala Leu Thr Val Leu	1085	1090	1095
	Thr Leu Leu Gly Leu Leu His Gly Leu Val Leu Leu Pro Val Leu	1100	1105	1110
25	Leu Ser Ile Leu Gly Pro Pro Pro Glu Val Ile Gln Met Tyr Lys	1115	1120	1125
	Glu Ser Pro Glu Ile Leu Ser Pro Pro Ala Pro Gln Gly Gly Gly	1130	1135	1140
30	Leu Arg Trp Gly Ala Ser Ser Ser Leu Pro Gln Ser Phe Ala Arg	1145	1150	1155
35	Val Thr Thr Ser Met Thr Val Ala Ile His Pro Pro Pro Leu Pro	1160	1165	1170
	Gly Ala Tyr Ile His Pro Ala Pro Asp Glu Pro Pro Trp Ser Pro	1175	1180	1185
40	Ala Ala Thr Ser Ser Gly Asn Leu Ser Ser Arg Gly Pro Gly Pro	1190	1195	1200
45	Ala Thr Gly	1203		
	<210> 3			
	<211> 228			
	<212> DNA			
50	<213> Homo sapiens			
	<220>			
	<221> unknown			
	<222> 20, 27, 135, 156, 210			
	<223> unknown base			
55	<400> 3			
	gctggggtgc acgcctacn cagcggntcc ccttctctct tctgggaaca			50
60	gtatctgggc ctgcggcgct gcttctctgct ggccgtctgc atctgtctgg			100
	tgtgcacttt cctcgtctgt gctctgctgc tctnaaccc ctggacggct			150

ggcctnatag tgctgggtcct ggcgatgatg acagtgaac tctttggtat 200

catgggtttt ctgggcatca agctgagt 228

5

<210> 4  
<211> 76  
<212> PRT  
<213> Homo sapiens

10

<400> 4  
Leu Gly Leu Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp  
1 5 10 15

15

Glu Gln Tyr Ile Gly Leu Arg His Trp Leu Leu Leu Phe Ile Ser  
20 25 30

20

Val Val Leu Ala Cys Thr Phe Leu Val Cys Ala Val Phe Leu Leu  
35 40 45

Asn Pro Trp Thr Ala Gly Ile Ile Val Met Val Leu Ala Leu Met  
50 55 60

25

Thr Val Glu Leu Phe Gly Met Met Gly Leu Ile Gly Ile Lys Leu  
65 70 75

Ser  
76

30

<210> 5  
<211> 125  
<212> DNA  
<213> Homo sapiens

35

<220>  
<221> unknown  
<222> 115  
<223> unknown base

40

<400> 5  
gctgggggtgc acgcctaccc cagcggtcc cccttcctct tctgggaaca 50

gtatctgggc ctgcggcgct gcttcctgct ggccgtctgc atcctgctgg 100

45

tgtgcacttt cctcntctgt gctct 125

<210> 6  
<211> 50  
<212> DNA  
<213> Homo sapiens

50

<220>  
<221> unknown  
<222> 13-14  
<223> unknown base

55

<400> 6  
ccggcgggca tgnngcgaag cggaccacgc tgggggggtgg ctcaggggag 50

60

<210> 7  
<211> 1182

<212> PRT  
 <213> Mus musculus

<400> 7

5	Met	Val	Arg	Pro	Leu	Ser	Leu	Gly	Glu	Leu	Pro	Pro	Ser	Tyr	Thr	1	5	10	15
	Pro	Pro	Ala	Arg	Ser	Ser	Ala	Pro	His	Ile	Leu	Ala	Gly	Ser	Leu	20	25	30	
10	Gln	Ala	Pro	Leu	Trp	Leu	Arg	Ala	Tyr	Phe	Gln	Gly	Leu	Leu	Phe	35	40	45	
15	Ser	Leu	Gly	Cys	Arg	Ile	Gln	Lys	His	Cys	Gly	Lys	Val	Leu	Phe	50	55	60	
	Leu	Gly	Leu	Val	Ala	Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Arg	Val	65	70	75	
20	Ala	Val	Ile	Glu	Thr	Asp	Leu	Glu	Gln	Leu	Trp	Val	Glu	Val	Gly	80	85	90	
	Ser	Arg	Val	Ser	Gln	Glu	Leu	His	Tyr	Thr	Lys	Glu	Lys	Leu	Gly	95	100	105	
25	Glu	Glu	Ala	Ala	Tyr	Thr	Ser	Gln	Met	Leu	Ile	Gln	Thr	Ala	His	110	115	120	
30	Gln	Glu	Gly	Gly	Asn	Val	Leu	Thr	Pro	Glu	Ala	Leu	Asp	Leu	His	125	130	135	
	Leu	Gln	Ala	Ala	Leu	Thr	Ala	Ser	Lys	Val	Gln	Val	Ser	Leu	Tyr	140	145	150	
35	Gly	Lys	Ser	Trp	Asp	Leu	Asn	Lys	Ile	Cys	Tyr	Lys	Ser	Gly	Val	155	160	165	
	Pro	Leu	Ile	Glu	Asn	Gly	Met	Ile	Glu	Arg	Met	Ile	Glu	Lys	Leu	170	175	180	
40	Phe	Pro	Cys	Val	Ile	Leu	Thr	Pro	Leu	Asp	Cys	Phe	Trp	Glu	Gly	185	190	195	
45	Ala	Lys	Leu	Gln	Gly	Gly	Ser	Ala	Tyr	Leu	Pro	Gly	Arg	Pro	Asp	200	205	210	
	Ile	Gln	Trp	Thr	Asn	Leu	Asp	Pro	Gln	Gln	Leu	Leu	Glu	Glu	Leu	215	220	225	
50	Gly	Pro	Phe	Ala	Ser	Leu	Glu	Gly	Phe	Arg	Glu	Leu	Leu	Asp	Lys	230	235	240	
	Ala	Gln	Val	Gly	Gln	Ala	Tyr	Val	Gly	Arg	Pro	Cys	Leu	Asp	Pro	245	250	255	
55	Asp	Asp	Pro	His	Cys	Pro	Pro	Ser	Ala	Pro	Asn	Arg	His	Ser	Arg	260	265	270	
60	Gln	Ala	Pro	Asn	Val	Ala	Gln	Glu	Leu	Ser	Gly	Gly	Cys	His	Gly	275	280	285	



Patent # 9,400,660

	Glu	Gln	Ala	Ser	Met	Val	Leu	Gln	Ala	Trp	Gln	Arg	Arg	Phe	Val
					350					355					360
5	Gln	Leu	Ala	Gln	Glu	Ala	Leu	Pro	Ala	Asn	Ala	Ser	Gln	Gln	Ile
					365					370					375
	His	Ala	Phe	Ser	Ser	Thr	Thr	Leu	Asp	Asp	Ile	Leu	Arg	Ala	Phe
					380					385					390
10	Ser	Glu	Val	Ser	Thr	Thr	Arg	Val	Val	Gly	Gly	Tyr	Leu	Leu	Met
					395					400					405
	Leu	Ala	Tyr	Ala	Cys	Val	Thr	Met	Leu	Arg	Trp	Asp	Cys	Ala	Gln
15					410					415					420
	Ser	Gln	Gly	Ala	Val	Gly	Leu	Ala	Gly	Val	Leu	Leu	Val	Ala	Leu
					425					430					435
20	Ala	Val	Ala	Ser	Gly	Leu	Gly	Leu	Cys	Ala	Leu	Leu	Gly	Ile	Thr
					440					445					450
	Phe	Asn	Ala	Ala	Thr	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly
					455					460					465
25	Ile	Gly	Val	Asp	Asp	Ile	Phe	Leu	Leu	Ala	His	Ala	Phe	Thr	Lys
					470					475					480
	Ala	Pro	Pro	Asp	Thr	Pro	Leu	Pro	Glu	Arg	Met	Gly	Glu	Cys	Leu
30					485					490					495
	Arg	Ser	Thr	Gly	Thr	Ser	Val	Ala	Leu	Thr	Ser	Val	Asn	Asn	Met
					500					505					510
35	Val	Ala	Phe	Phe	Met	Ala	Ala	Leu	Val	Pro	Ile	Pro	Ala	Leu	Arg
					515					520					525
	Ala	Phe	Ser	Leu	Gln	Ala	Ala	Ile	Val	Val	Gly	Cys	Asn	Phe	Ala
					530					535					540
40	Ala	Val	Met	Leu	Val	Phe	Pro	Ala	Ile	Leu	Ser	Leu	Asp	Leu	Arg
					545					550					555
	Arg	Arg	His	Arg	Gln	Arg	Leu	Asp	Val	Leu	Cys	Cys	Phe	Ser	Ser
45					560					565					570
	Pro	Cys	Ser	Ala	Gln	Val	Ile	Gln	Met	Leu	Pro	Gln	Glu	Leu	Gly
					575					580					585

0990044660  
"T" 1002

	Asp Arg Ala Val	Pro Val Gly Ile Ala	His Leu Thr Ala Thr	Val
		590	595	600
5	Gln Ala Phe Thr	His Cys Glu Ala Ser	Ser Gln His Val Val	Thr
		605	610	615
	Ile Leu Pro Pro	Gln Ala His Leu Leu	Ser Pro Ala Ser Asp	Pro
		620	625	630
10	Leu Gly Ser Glu	Leu Tyr Ser Pro Gly	Gly Ser Thr Arg Asp	Leu
		635	640	645
	Leu Ser Gln Glu	Glu Gly Thr Gly Pro	Gln Ala Ala Cys Arg	Pro
		650	655	660
15	Leu Leu Cys Ala	His Trp Thr Leu Ala	His Phe Ala Arg Tyr	Gln
		665	670	675
20	Phe Ala Pro Leu	Leu Leu Gln Thr Arg	Ala Lys Ala Leu Val	Leu
		680	685	690
	Leu Phe Phe Gly	Ala Leu Leu Gly Leu	Ser Leu Tyr Gly Ala	Thr
		695	700	705
25	Leu Val Gln Asp	Gly Leu Ala Leu Thr	Asp Val Val Pro Arg	Gly
		710	715	720
	Thr Lys Glu His	Ala Phe Leu Ser Ala	Gln Leu Arg Tyr Phe	Ser
		725	730	735
30	Leu Tyr Glu Val	Ala Leu Val Thr Gln	Gly Gly Phe Asp Tyr	Ala
		740	745	750
35	His Ser Gln Arg	Ala Leu Phe Asp Leu	His Gln Arg Phe Ser	Ser
		755	760	765
	Leu Lys Ala Val	Leu Pro Pro Pro Ala	Thr Gln Ala Pro Arg	Thr
		770	775	780
40	Trp Leu His Tyr	Tyr Arg Ser Trp Leu	Gln Gly Ile Cln Ala	Ala
		785	790	795
	Phe Asp Gln Asp	Trp Ala Ser Gly Arg	Ile Thr Cys His Ser	Tyr
		800	805	810
45	Arg Asn Gly Ser	Glu Asp Gly Ala Leu	Ala Tyr Lys Leu Leu	Ile
		815	820	825



09900465-13001  
"T002T" 91906660

	Gln Thr Gly Asn Ala Gln Glu Pro Leu Asp Phe Ser Gln Leu Thr	830	835	840
5	Thr Arg Lys Leu Val Asp Lys Glu Gly Leu Ile Pro Pro Glu Leu	845	850	855
	Phe Tyr Met Gly Leu Thr Val Trp Val Ser Ser Asp Pro Leu Gly	860	865	870
10	Leu Ala Ala Ser Gln Ala Asn Phe Tyr Pro Pro Pro Pro Glu Trp	875	880	885
	Leu His Asp Lys Tyr Asp Thr Thr Gly Glu Asn Leu Arg Ile Pro	890	895	900
15	Ala Ala Gln Pro Leu Glu Phe Ala Gln Phe Pro Phe Leu Leu His	905	910	915
	Gly Leu Gln Lys Thr Ala Asp Phe Val Glu Ala Ile Glu Gly Ala	920	925	930
20	Arg Ala Ala Cys Thr Glu Ala Gly Gln Ala Gly Val His Ala Tyr	935	940	945
	Pro Ser Gly Ser Pro Phe Leu Phe Trp Glu Gln Tyr Leu Gly Leu	950	955	960
25	Arg Arg Cys Phe Leu Leu Ala Val Cys Ile Leu Leu Val Cys Thr	965	970	975
30	Phe Leu Val Cys Ala Leu Leu Leu Leu Ser Pro Trp Thr Ala Gly	980	985	990
	Leu Ile Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly	995	1000	1005
35	Ile Met Gly Phe Leu Gly Ile Lys Leu Ser Ala Ile Pro Val Val	1010	1015	1020
	Ile Leu Val Ala Ser Ile Gly Ile Gly Val Glu Phe Thr Val His	1025	1030	1035
40	Val Ala Leu Gly Phe Leu Thr Ser His Gly Ser Arg Asn Leu Arg	1040	1045	1050
45	Ala Ala Ser Ala Leu Glu Gln Thr Phe Ala Pro Val Thr Asp Gly	1055	1060	1065

Ala Val Ser Thr Leu Leu Gly Leu Leu Met Leu Ala Gly Ser Asn  
1070 1075 1080

5 Phe Asp Phe Ile Ile Arg Tyr Phe Phe Val Val Leu Thr Val Leu  
1085 1090 1095

Thr Leu Leu Gly Leu Leu His Gly Leu Leu Leu Leu Pro Val Leu  
1100 1105 1110

10 Leu Ser Ile Leu Gly Pro Pro Pro Gln Val Val Gln Val Tyr Lys  
1115 1120 1125

Glu Ser Pro Gln Thr Leu Asn Ser Ala Ala Pro Gln Arg Gly Gly  
1130 1135 1140

15 Leu Arg Trp Asp Arg Pro Pro Thr Leu Pro Gln Ser Phe Ala Arg  
1145 1150 1155

20 Val Thr Thr Ser Met Thr Val Ala Leu His Pro Pro Pro Leu Pro  
1160 1165 1170

Gly Ala Tyr Val His Pro Ala Ser Glu Glu Pro Thr  
1175 1180 1182

25 <210> 8  
<211> 4004  
<212> DNA  
<213> Homo sapiens

30 <400> 8  
ccacgcgctc cgggagaagc tgggggagga ggctgcatac acctctcaga 50  
tgctgataca gaccgcacgc caggagggag agaacatcct cacacccgaa 100  
35 gcaacttgcc tccacctcca ggcagccctc actgccagta aagtccaagt 150  
atcactctat gggaagtcct gggatttgaa caaaatctgc tacaagtcag 200  
gagttcccct tattgaaaat ggaatgattg agcggatgat tgagaagctg 250  
40 tttccgtgcg tgatcctcac cccctcgac tgcttctggg agggagccaa 300  
actccaaggg ggctccgctt acctgccgct cccaatgtgg ctcacgagct 350  
45 gagggtgggc tgccatggct tctcccacaa attcatgcac tggcaggagg 400  
aattgctgct gggaggcatg gccagagacc cccaaggaga gctgctgagg 450  
gcagaggccc tgcagagcac cttcttgctg atgagtcacc gccagctgta 500  
50 cgagcatttc cggggtgact atcagacaca tgacattggc tggagtgagg 550  
agcaggccag cacagtgcct caagcctggc agcggcgctt tgtgcaggctc 600  
55 ggtatggaca aggacagggg ggtgccctga ggccattccc tcctcctgcc 650  
ccctcctatc caccctgttt ctccagctgg cccaggaggc cctgcctgag 700  
aacgcttccc agcagatcca tgccttctcc tccaccaccc tggatgacat 750  
60 cctgcatgcg ttctctgaag tcagtgtctc ccgtgtggtg ggaggctatc 800

5

10

15

20

25

30

35

40

45

50

55

60

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60

atgtggtgcc tgggggcacc aaggagcatg ccttcctgag cgcccagctc 2350  
 aggtacttct cctgtacga ggtggccctg gtgaccaggt gtggctttga 2400  
 ctacgcccac tcccaacgcg cctcttttga tctgcaccag cgcttcagtt 2450  
 ccctcaaggc ggtgctgccc ccaccggcca ccagggcacc ccgcacctgg 2500  
 ctgcactatt accgcaactg gctacaggga atccaggctg cctttgacca 2550  
 ggactgggct tctggggcga tcaccgcca ctcgtagcgc aatggctctg 2600  
 aggatggggc cctggcctac aagctgctca tccagactgg agacgcccag 2650  
 gagcctctgg atttcagcca ggttgggaga gggctggagg ggtccactag 2700  
 tacaggggct gcaggcctcc tggggccagg ccttcagccc tctctgcctc 2750  
 tgcagctgac cacaaggaag ctggtggaca gagagggact gattccaccc 2800  
 gagctcttct acatggggct gaccgtgtgg gtgagcagtg acccctggg 2850  
 tctggcagcc tcacaggcca acttctaccc ccacctcct gaatggctgc 2900  
 acgacaaata cgacaccacg ggggagaacc ttgcagtgga gtcttggggg 2950  
 gagctcggca agagcctcag cctcgcccac acaagccctg agcctgaggc 3000  
 cctgcccact ctgccccgtg ctacccgccc tgtccctctc cctcttctcc 3050  
 cttccctctc cctccacagt ccgcccagct cagcccttgg agtttgcca 3100  
 gttcccttct ctgctgcgtg gcctccagaa gactgcagac tttgtggagg 3150  
 ccatcgaggg ggcccgggca gcatgcccag aggcgggcca ggctgggggtg 3200  
 cagcctacc ccagcggctc ccccttctc ttctgggaac agtatctggg 3250  
 cctgcggcgc tgettctctg tggccgtctg catcctgctg gtgtgcactt 3300  
 tctcgtctg tgcctctgct ctcccaacc cctggacggc tggcctcata 3350  
 gtgagtgtt gcaggagtgg ggacagagac accccaccct tccctgcca 3400  
 gcctgtcatc cctcctgcca ggagccctct gtgagccctg tctccctcag 3450  
 gtgctggtcc tggcgatgat gacagtggaa ctctttggta tcatgggttt 3500  
 cctgggcata aagctgagtg ccatcccggt ggtgacctt gtggcctctg 3550  
 taggcattgg cgctgagttc acagtccacg tggctctggg gagcacgggc 3600  
 accccgggga gggaccaatc agctgattca gtattcaaca catattgttc 3650  
 aagcccctac tatgtgctag gtactattta agaatttggg ctgggtggac 3700  
 gtgggtggctc attcctgtaa tcccagcact ttgggaggcc gaggcgggtg 3750  
 gatcacctga ggtcgggagt tcgaaaccag cctggccaac atggtgaaac 3800  
 cctgtcttta ctaaaaatac aaaaaattag ccaggcgtgg tggcacatgc 3850

T0021-400560

cagtagtccc agctactttg gaggctgagg cagaattgct tgaacctggg 3900  
 aggcgaaggt tgcagtgagc tgagatcgtg ccattgcact ccagcctggg 3950  
 5 caacaagagt gcaactctcc gtctcaaaaa aaaaaaaaaa aagggcggcc 4000  
 gcga 4004  
 10 <210> 9  
 <211> 2082  
 <212> DNA  
 <213> Homo sapiens  
 15 <400> 9  
 ttccggcatg actcgatcgc cgccctcag agagctgccc ccgagttaca 50  
 cccccccagc tcgaaccgca gcacccaga tcctagctgg gagcctgaag 100  
 20 gctccactct ggcttcgtgc ttacttccag ggctgctct tctctctggg 150  
 atgcgggatc cagagacatt gtggcaagt gctctttctg ggactgttgg 200  
 cctttggggc cctggcatta ggtctccgca tggccattat tgagacaaac 250  
 25 ttggaacagc tctgggtaga agtgggcagc cgggtgagcc aggagctgca 300  
 ttacaccaag gagaagctgg gggaggaggc tgcatacacc tctcagatgc 350  
 30 tgatacagac cgcacgccag gagggagaga acatcctcac acccgaagca 400  
 cttggcctcc acctccaggc agccctcact gccagtaaag tccaagtatc 450  
 actctatggg aagtccctggg atttgaacaa aatctgctac aagtcaggag 500  
 35 ttcccottat tgaaaatgga atgattgagt ggatgattga gaagctgttt 550  
 ccgtgctgta tctcacccc cctcgactgc ttctgggagg gagccaaact 600  
 40 ccaagggggc tccgcctacc tgcccggccg cccggatata cagtggacca 650  
 acctggatcc agagcagctg ctggaggagc tgggtccctt tgcctccctt 700  
 gagggccttc gggagctgct agacaaggca cagggtgggccc aggcctacgt 750  
 45 ggggcggccc tgtctgcacc ctgatgacct ccactgccca cctagtgcc 800  
 ccaaccatca cagcaggcag gctcccaatg tggctcacga gctgagtggg 850  
 50 ggctgccatg gcttctccca caaattcatg cactggcagg aggaattgct 900  
 gctgggaggc atggccagag acccccaagg agagctgctg agggcagagg 950  
 ccctgcagag caccttcttg ctgatgagtc cccgccagct gtacgagcat 1000  
 55 ttccgggggtg actatcagac acatgacatt ggctggagtg aggagcaggc 1050  
 cagcacagtg ctacaagcct ggcagcggcg ctttgtgcag ctggcccagg 1100  
 60 aggcctgccc tgagaacgct tcccagcaga tccatgcctt ctctccacc 1150

```

    <210> 10  

40   <211> 1315  

     <212> PRT  

     <213> Homo sapiens  
  

    <400> 10  

45   Met Glu Lys Tyr His Val Leu Glu Met Ile Gly Glu Gly Ser Phe  

      1           5          10         15  
  

     Gly Arg Val Tyr Lys Gly Arg Arg Lys Tyr Ser Ala Gln Val Val  

                        20       25        30  
  

50   Ala Leu Lys Phe Ile Pro Lys Leu Gly Arg Ser Glu Lys Glu Leu  

                      35          40        45  
  

     Arg Asn Leu Gln Arg Glu Ile Glu Ile Met Arg Gly Leu Arg His  

                    50          55        60  
  

55   Pro Asn Ile Val His Met Leu Asp Ser Phe Glu Thr Asp Lys Glu  

                     65          70        75  
  

60   Val Val Val Val Thr Asp Tyr Ala Glu Gly Glu Leu Phe Gln Ile  

                   80          85        90
```

5

10

15

20

25

30

35

Patent # 9,400,650

	Thr	Pro	Phe	Thr	Ser	Arg	Leu	Pro	Pro	Glu	Leu	Gln	Val	Leu	Lys
					275					280					285
5	Asp	Glu	Gln	Ala	His	Arg	Leu	Ala	Pro	Lys	Gly	Asn	Gln	Ser	Arg
					290					295					300
	Ile	Leu	Thr	Gln	Ala	Tyr	Lys	Arg	Met	Ala	Glu	Glu	Ala	Met	Gln
					305					310					315
10	Lys	Lys	His	Gln	Asn	Thr	Gly	Pro	Ala	Leu	Glu	Gln	Glu	Asp	Lys
					320					325					330
	Thr	Ser	Lys	Val	Ala	Pro	Gly	Thr	Ala	Pro	Leu	Pro	Arg	Leu	Gly
					335					340					345
15	Ala	Thr	Pro	Gln	Glu	Ser	Ser	Leu	Leu	Ala	Gly	Ile	Leu	Ala	Ser
					350					355					360
20	Glu	Leu	Lys	Ser	Ser	Trp	Ala	Lys	Ser	Gly	Thr	Gly	Glu	Val	Pro
					365					370					375
	Ser	Ala	Pro	Arg	Glu	Asn	Arg	Thr	Thr	Pro	Asp	Cys	Glu	Arg	Ala
					380					385					390
25	Phe	Pro	Glu	Glu	Arg	Pro	Glu	Val	Leu	Gly	Gln	Arg	Ser	Thr	Asp
					395					400					405
	Val	Val	Asp	Leu	Glu	Asn	Glu	Glu	Pro	Asp	Ser	Asp	Asn	Glu	Trp
					410					415					420
30	Gln	His	Leu	Leu	Glu	Thr	Thr	Glu	Pro	Val	Pro	Ile	Gln	Leu	Lys
					425					430					435
	Ala	Pro	Leu	Thr	Leu	Leu	Cys	Asn	Pro	Asp	Phe	Cys	Gln	Arg	Ile
					440					445					450
35	Gln	Ser	Gln	Leu	His	Glu	Ala	Gly	Gly	Gln	Ile	Leu	Lys	Gly	Ile
					455					460					465
40	Leu	Glu	Gly	Ala	Ser	His	Ile	Leu	Pro	Ala	Phe	Arg	Val	Leu	Ser
					470					475					480
	Ser	Leu	Leu	Ser	Ser	Cys	Ser	Asp	Ser	Val	Ala	Leu	Tyr	Ser	Phe
					485					490					495
45	Cys	Arg	Glu	Ala	Gly	Leu	Pro	Gly	Leu	Leu	Leu	Ser	Leu	Leu	Arg
					500					505					510



5

10

15

20

25

30

35

40

45

Pro Leu Ala Leu Glu Ser Leu Phe Met Leu Ile Gln Gly Lys Val  
740 745 750

0990046-12001  
T00271-9400660

	Lys Val Val Asp Trp Glu Glu Ser Thr Glu Val Thr Leu Tyr Phe	755	760	765
5	Leu Ser Leu Leu Val Phe Arg Leu Gln Asn Leu Pro Cys Gly Met	770	775	780
	Glu Lys Leu Gly Ser Asp Val Ala Thr Leu Phe Thr His Ser His	785	790	795
10	Val Val Ser Leu Val Ser Ala Ala Ala Cys Leu Leu Gly Gln Leu	800	805	810
	Gly Gln Gln Gly Val Thr Phe Asp Leu Gln Pro Met Glu Trp Met	815	820	825
15	Ala Ala Ala Thr His Ala Leu Ser Ala Pro Ala Glu Val Arg Leu	830	835	840
20	Thr Pro Pro Gly Ser Cys Gly Phe Tyr Asp Gly Leu Leu Ile Leu	845	850	855
	Leu Leu Gln Leu Leu Thr Glu Gln Gly Lys Ala Ser Leu Ile Arg	860	865	870
25	Asp Met Ser Ser Ser Glu Met Trp Thr Val Leu Trp His Arg Phe	875	880	885
	Ser Met Val Leu Arg Leu Pro Glu Glu Ala Ser Ala Gln Glu Gly	890	895	900
30	Glu Leu Ser Leu Ser Ser Pro Pro Ser Pro Glu Pro Asp Trp Thr	905	910	915
35	Leu Ile Ser Pro Gln Gly Met Ala Ala Leu Leu Ser Leu Ala Met	920	925	930
	Ala Thr Phe Thr Gln Glu Pro Gln Leu Cys Leu Ser Cys Leu Ser	935	940	945
40	Gln His Gly Ser Ile Leu Met Ser Ile Leu Lys His Leu Leu Cys	950	955	960
	Pro Ser Phe Leu Asn Gln Leu Arg Gln Ala Pro His Gly Ser Glu	965	970	975
45	Phe Leu Pro Val Val Val Leu Ser Val Cys Gln Leu Leu Cys Phe	980	985	990

5

10

15

20

25

30

25

40

45

Leu Gly Asn Leu Gly Pro Glu Gly Leu Gly Glu Glu Leu Leu Glu  
1220 1225 1230

Cys Glu Val Pro Gln Arg Leu Leu Glu Met Ala Cys Gly Asp Pro  
 1235 1240 1245  
 5 Gln Pro Asn Val Lys Glu Ala Ala Leu Ile Ala Leu Arg Ser Leu  
 1250 1255 1260  
 Gln Gln Glu Pro Gly Ile His Gln Val Leu Val Ser Leu Gly Ala  
 1265 1270 1275  
 10 Ser Glu Lys Leu Ser Leu Leu Ser Leu Gly Asn Gln Ser Leu Pro  
 1280 1285 1290  
 His Ser Ser Pro Arg Pro Ala Ser Ala Lys His Cys Arg Lys Leu  
 1295 1300 1305  
 15 Ile His Leu Leu Arg Pro Ala His Ser Met  
 1310 1315  
 20 <210> 11  
 <211> 48  
 <212> DNA  
 <213> Artificial sequence  
 25 <220>  
 <223> Artificial sequence 1-48  
 <400> 11  
 ctatgaaatt aaccctcact aaaggagct cccgtgagtc cctatgtg 48  
 30 <210> 12  
 <211> 48  
 <212> DNA  
 <213> Artificial sequence  
 35 <220>  
 <223> Artificial sequence 1-48  
 <400> 12  
 ggattctaatt acgactcact atagggcccc taaactccgc tgctccac 48  
 40 <210> 13  
 <211> 396  
 <212> PRT  
 <213> Mus musculus  
 45 <400> 13  
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu  
 1 5 10 15  
 50 Leu Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val  
 20 25 30  
 Gly Arg Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr  
 35 40 45  
 55 Lys Gln Phe Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser  
 50 55 60  
 60 Gly Pro Ala Glu Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg  
 65 70 75

	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu
					80					85					90
5	Glu	Asn	Ser	Gly	Ala	Asp	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu
					95					100					105
	Arg	Val	Asn	Ala	Leu	Ala	Ile	Ala	Val	Met	Asn	Met	Trp	Pro	Gly
					110					115					120
10	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His
					125					130					135
	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Leu	Asp	Ile	Thr
					140					145					150
15	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu
					155					160					165
	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Arg	Asn
20					170					175					180
	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	Ala	Val	Arg
					185					190					195
25	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	Arg	Ser
					200					205					210
	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	Val
					215					220					225
30	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu
					230					235					240
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala
35					245					250					255

4:

5

10

15

20

25

30

35

40

45

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu  
230 235 240

Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val  
245 250 255

Ile Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala  
260 265 270

His Leu Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro  
275 280 285

Gly Pro Ser Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg  
290 295 300

Sequence "T000000000"

	Val	Tyr	Val	Val	Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	
					305					310					315	
5	Ala	Ala	Val	His	Ser	Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	
					320					325					330	
	Tyr	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	
					335					340					345	
10	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	
					350					355					360	
	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His	Ala	Leu	Leu	Ala	Ala	
					365					370					375	
15	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly	Gly	Gly	Gly	Ser	Ile	Pro	
					380					385					390	
	Ala	Ala	Gln	Ser	Ala	Thr	Glu	Ala	Arg	Gly	Ala	Glu	Pro	Thr	Ala	
20					395					400					405	
	Gly	Ile	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	His	Ile	Gly	Thr	Trp	
					410					415					420	
25	Leu	Leu	Asp	Ser	Glu	Thr	Met	His	Pro	Leu	Gly	Met	Ala	Val	Lys	
					425					430					435	
	Ala	Ser														
		437														
30	<210>	15														
	<211>	803														
	<212>	PRT														
	<213>	Artificial sequence														
35	<220>															
	<223>	Artificial sequence 1-803														
	<400>	15														
40	Met	Ala	Ala	Gly	Arg	Pro	Val	Arg	Cly	Pro	Glu	Leu	Ala	Pro	Arg	
	1				5					10					15	
	Arg	Leu	Leu	Gln	Leu	Leu	Leu	Leu	Val	Leu	Leu	Gly	Gly	Arg	Gly	
					20					25					30	
45	Arg	Gly	Ala	Ala	Leu	Ser	Gly	Asn	Val	Thr	Gly	Pro	Gly	Pro	Arg	
					35					40					45	



5

10

15

20

25

30

35

40

45

5

10

15

20

25

30

25

- 40

45

0500044-94006660  
 Patent # 9,400,666

	Leu Phe Ala Met Phe Gly Thr Gly Ile Ala Met Ser Thr Trp Val	
	530	540
5	Trp Thr Lys Ala Thr Leu Leu Ile Trp Arg Arg Thr Trp Cys Arg	
	545	555
	Leu Thr Gly His Ser Asp Asp Glu Pro Lys Arg Ile Lys Lys Ser	
	560	570
10	Lys Met Ile Ala Lys Ala Phe Ser Lys Arg Arg Glu Leu Leu Gln	
	575	585
	Asn Pro Gly Gln Glu Leu Ser Phe Ser Met His Thr Val Ser His	
	590	600
15	Asp Gly Pro Val Ala Gly Leu Ala Phe Glu Leu Asn Glu Pro Ser	
	605	615
20	Ala Asp Val Ser Ser Ala Trp Ala Gln His Val Thr Lys Met Val	
	620	630
	Ala Arg Arg Gly Ala Ile Leu Pro Gln Asp Val Ser Val Thr Pro	
	635	645
25	Val Ala Thr Pro Val Pro Pro Glu Glu Gln Ala Asn Leu Trp Leu	
	650	660
	Val Glu Ala Glu Ile Ser Pro Glu Leu Glu Lys Arg Leu Gly Arg	
	665	675
30	Lys Lys Lys Arg Arg Lys Arg Lys Lys Glu Val Cys Pro Leu Gly	
	680	690
	Pro Ala Pro Glu Leu His His Ser Ala Pro Val Pro Ala Thr Ser	
	695	705
35	Ala Val Pro Arg Leu Pro Gln Leu Pro Arg Gln Lys Cys Leu Val	
	710	720
40	Ala Ala Asn Ala Trp Gly Thr Gly Glu Pro Cys Arg Gln Gly Ala	
	725	735
	Trp Thr Val Val Ser Asn Pro Phe Cys Pro Glu Pro Ser Pro His	
	740	750
45	Gln Asp Pro Phe Leu Pro Gly Ala Ser Ala Pro Arg Val Trp Ala	
	755	765

09990046-12001  
T0022T-9400660

	Gln Gly Arg Leu	Gln Gly Leu Gly Ser	Ile His Ser Arg Thr	Asn
		770	775	780
5	Leu Met Glu Ala	Glu Leu Leu Asp Ala	Asp Ser Asp Phe Glu	Gln
		785	790	795
	Lys Leu Ile Ser	Glu Glu Asp Leu		
		800	803	
10	<210> 16			
	<211> 793			
	<212> PRT			
	<213> Artificial sequence			
15	<220>			
	<223> Artificial sequence 1-793			
	<400> 16			
20	Met Ala Ala Gly Arg	Pro Val Arg Gly	Pro Glu Leu Ala	Pro Arg
	1	5	10	15
	Arg Leu Leu Gln	Leu Leu Leu Val	Leu Leu Gly Gly	Arg Gly
		20	25	30
25	Arg Gly Ala Ala	Leu Ser Gly Asn Val	Thr Gly Pro Gly	Pro Arg
		35	40	45
	Ser Ala Gly Gly	Ser Ala Arg Arg	Asn Ala Pro Val	Thr Ser Pro
		50	55	60
30	Pro Pro Pro Leu	Leu Ser His Cys	Gly Arg Ala Ala	His Cys Glu
		65	70	75
	Pro Leu Arg Tyr	Asn Val Cys Leu	Gly Ser Ala Leu	Pro Tyr Gly
35		80	85	90
	Ala Thr Thr Thr	Leu Leu Ala Gly	Asp Ser Asp Ser	Gln Glu Glu
		95	100	105
40	Ala His Ser Lys	Leu Val Leu Trp	Ser Gly Leu Arg	Asn Ala Pro
		110	115	120
	Arg Cys Trp Ala	Val Ile Gln Pro	Leu Leu Cys Ala	Val Tyr Met
		125	130	135
45	Pro Lys Cys Glu	Asn Asp Arg Val	Glu Leu Pro Ser	Arg Thr Leu
		140	145	150

5

10

15

20

25

30

35

40

45

0990046-112001

	Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr Arg Ala	395	400	405
5	Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu Ile Val Gly Gly	410	415	420
	Tyr Phe Leu Ile Arg Gly Val Met Thr Leu Phe Ser Ile Lys Ser	425	430	435
10	Asn His Pro Gly Leu Leu Ser Glu Lys Ala Ala Ser Lys Ile Asn	440	445	450
	Glu Thr Met Leu Arg Leu Gly Ile Phe Gly Phe Leu Ala Phe Gly	455	460	465
15	Phe Val Leu Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn	470	475	480
	Gln Ala Glu Trp Glu Arg Ser Phe Arg Asp Tyr Val Leu Cys Gln	485	490	495
20	Ala Asn Val Thr Ile Gly Leu Pro Thr Lys Lys Pro Ile Pro Asp	500	505	510
	Cys Glu Ile Lys Asn Arg Pro Ser Leu Leu Val Glu Lys Ile Asn	515	520	525
	Leu Phe Ala Met Phe Gly Thr Gly Ile Ala Met Ser Thr Leu Val	530	535	540
30	Trp Thr Lys Ala Thr Leu Leu Ile Trp Arg Arg Thr Trp Cys Arg	545	550	555
	Leu Thr Gly His Ser Asp Asp Glu Pro Lys Arg Ile Lys Lys Ser	560	565	570
35	Lys Met Ile Ala Lys Ala Phe Ser Lys Arg Arg Glu Leu Leu Gln	575	580	585
	Asn Pro Gly Gln Glu Leu Ser Phe Ser Met His Thr Val Ser His	590	595	600
	Asp Gly Pro Val Ala Gly Leu Ala Phe Glu Leu Asn Glu Pro Ser	605	610	615
45	Ala Asp Val Ser Ser Ala Trp Ala Gln His Val Thr Lys Met Val	620	625	630

09990045-11001

	Ala	Arg	Arg	Gly	Ala	Ile	Leu	Pro	Gln	Asp	Val	Ser	Val	Thr	Pro	
					635					640					645	
5	Val	Ala	Thr	Pro	Val	Pro	Pro	Glu	Glu	Gln	Ala	Asn	Leu	Trp	Leu	
					650					655					660	
	Val	Glu	Ala	Glu	Ile	Ser	Pro	Glu	Leu	Glu	Lys	Arg	Leu	Gly	Arg	
					665					670					675	
10	Lys	Lys	Lys	Arg	Arg	Lys	Arg	Lys	Lys	Glu	Val	Cys	Pro	Leu	Gly	
					680					685					690	
	Pro	Ala	Pro	Glu	Leu	His	His	Ser	Ala	Pro	Val	Pro	Ala	Thr	Ser	
					695					700					705	
15	Ala	Val	Pro	Arg	Leu	Pro	Gln	Leu	Pro	Arg	Gln	Lys	Cys	Leu	Val	
					710					715					720	
20	Ala	Ala	Asn	Ala	Trp	Gly	Thr	Gly	Glu	Pro	Cys	Arg	Gln	Gly	Ala	
					725					730					735	
	Trp	Thr	Val	Val	Ser	Asn	Pro	Phe	Cys	Pro	Glu	Pro	Ser	Pro	His	
					740					745					750	
25	Gln	Asp	Pro	Phe	Leu	Pro	Gly	Ala	Ser	Ala	Pro	Arg	Val	Trp	Ala	
					755					760					765	
	Gln	Gly	Arg	Leu	Gln	Gly	Leu	Gly	Ser	Ile	His	Ser	Arg	Thr	Asn	
					770					775					780	
30	Leu	Met	Glu	Ala	Glu	Leu	Leu	Asp	Ala	Asp	Ser	Asp	Phe			
					785					790			793			
35	<210> 17															
	<211> 793															
	<212> PRT															
	<213> Homo sapiens															
40	<400> 17															
	Met	Ala	Ala	Gly	Arg	Pro	Val	Arg	Gly	Pro	Glu	Leu	Ala	Pro	Arg	
	1				5					10					15	
	Arg	Leu	Leu	Gln	Leu	Leu	Leu	Leu	Val	Leu	Leu	Gly	Gly	Arg	Gly	
					20					25					30	
45	Arg	Gly	Ala	Ala	Leu	Ser	Gly	Asn	Val	Thr	Gly	Pro	Gly	Pro	Arg	
					35					40					45	

5

10

15

20

25

30

35

40

43



Cys Glu Ile Lys Asn Arg Pro Ser Leu Leu Val Glu Lys Ile Asn  
515 520 525

4

Gln Gly Arg Leu Gln Gly Leu Gly Ser Ile His Ser Arg Thr Asn  
770 775 780

Leu Met Glu Ala Glu Leu Leu Asp Ala Asp Ser Asp Phe  
785 790 793

5

<210> 18  
<211> 228  
<212> DNA  
<213> Homo sapiens

10

<400> 18  
ctgggggctgt ccagttaccc caacggctac cccttcctct tctgggagca 50  
gtacatcggc ctccgccact ggctgctgct gttcatcagc gtggtgttgg 100  
cctgcacatt cctcgtgtgc gctgtcttcc ttctgaaccc ctggacggcc 150  
gggatcattg tgatggctct ggcgctgatg acggtcgagc tgttcggcat 200  
gatgggcctc atcggaatca agctcagt 228

15

20

<210> 19  
<211> 18  
<212> DNA  
<213> Homo sapiens

25

<400> 19  
aggcggggga tcacagca 18

30

<210> 20  
<211> 18  
<212> DNA  
<213> Homo sapiens

35

<400> 20  
ataccaaaga gttccact 18

40

<210> 21  
<211> 45  
<212> DNA  
<213> Artificial sequence

45

<220>  
<223> Artificial sequence 1-45

<400> 21  
ctgcggcgct gcttcctgct ggccgtctgc atcctgctgg tgtgc 45

50

<210> 22  
<211> 45  
<212> DNA  
<213> Artificial sequence

55

<220>  
<223> Artificial sequence 1-45

<400> 22  
agagcacaga cgaggaaagt gcacaccagc aggatgcaga cggcc 45

60

<210> 23

CGG90046-1001

<211> 21  
<212> DNA  
<213> Artificial sequence

5 <220>  
<223> Artificial sequence 1-21

<400> 23  
actcctgact tgtagcagat t 21

10 <210> 24  
<211> 21  
<212> DNA  
<213> Artificial sequence

15 <220>  
<223> Artificial sequence 1-21

20 <400> 24  
aggtgcata cacctctcag a 21

25 <210> 25  
<211> 18  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Artificial sequence 1-18

30 <400> 25  
gcttaggccc gaggagat 18

35 <210> 26  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Artificial sequence 1-20

40 <400> 26  
aactcacaac tttctctcca 20

45 <210> 27  
<211> 48  
<212> DNA  
<213> Artificial sequence

50 <220>  
<223> Artificial sequence 1-48

<400> 27  
ggattcctaat acgactcact atagggccca atggcctaaa ccgactgc 48

55 <210> 28  
<211> 46  
<212> DNA  
<213> Artificial sequence

60 <220>  
<223> Artificial sequence 1-46

<400> 28  
ctatgaaatt aaccctcact aaagggaccc acggcctctc ctcaca 46

5 <210> 29  
<211> 449  
<212> PRT  
<213> Mus musculus

10 <400> 29  
Met Glu Ser Pro Arg Ala Thr Gln Thr Pro Glu Ser Pro Lys Leu  
1 5 10 15  
15 Ser Gln Pro Arg Ala His Leu Ser Ala His Gln Ala Pro Ser Pro  
20 25 30  
Ala Ala Leu Pro Gly Tyr Pro Ala Met Ser Pro Ala Trp Leu Arg  
35 40 45  
20 Pro Arg Leu Arg Phe Cys Leu Phe Leu Leu Leu Leu Val  
50 55 60  
Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg Val Val Gly Ser Arg  
65 70 75  
25 Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys Gln Phe  
80 85 90  
Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr  
95 100 105  
30 Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr  
110 115 120  
35 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr  
125 130 135  
Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn  
140 145 150  
40 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu  
155 160 165  
45 Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu  
170 175 180  
Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp  
185 190 195  
50 Arg Asp Arg Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu  
200 205 210  
Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Val His  
215 220 225  
55 Cys Ser Val Lys Ser Glu His Ser Ala Ala Ala Lys Thr Gly Gly  
230 235 240  
Cys Phe Pro Ala Gly Ala Gln Val Arg Leu Glu Asn Gly Glu Arg  
245 250 255  
60

	Val	Ala	Leu	Ser	Ala	Val	Lys	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met
					260					265					270
5	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	Ser	Asp	Val	Leu	Ile	Phe	Leu
					275					280					285
	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	Phe	Gln	Val	Ile	Glu	Thr
					290					295					300
10	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	Pro	Ala	His	Leu	Leu
					305					310					315

09990046-12001  
T002T" 9400660

Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala His Phe Arg Ala  
320 325 330

5 Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val Ser  
335 340 345

Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr  
350 355 360

10 His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly Thr  
365 370 375

Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala  
380 385 390

15 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe  
395 400 405

20 Pro Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His  
410 415 420

Trp Tyr Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu  
425 430 435

25 Glu Ser Thr Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
440 445 449

<210> 30  
<211> 228  
<212> DNA  
<213> Homo sapiens

<400> 30  
ctggggctgt ccagttaccc caacggctac cccttcctct tctgggagca 50  
gtacatcggc ctccgccact ggctgctgct gttcatcagc gtggtgttgg 100  
cctgcacatt cctcgtgtgc gctgtcttcc ttctgaaccc ctggacggcc 150  
gggatcattg tgatggctct ggcgctgatg acggtcgagc tggtcggcat 200  
gatgggcctc atcggaatca agctcagt 228

<210> 31  
<211> 32  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Artificial sequence 1-32

<400> 31  
tcgacaagca gggaacaccc aagtagaagc tc 32

<210> 32  
<211> 32  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Artificial sequence 1-32

```
<400> 32
tcgacaagca ggggaagtggg aagtagaagc tc 32
```

5

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	6000
Health	0.5	0.5	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.4	0.5	0	1
Sleep	0.5	0.5	0	1
Appetite	0.5	0.5	0	1
Mood	0.5	0.5	0	1
Energy	0.5	0.5	0	1
Concentration	0.5	0.5	0	1
Memory	0.5	0.5	0	1
Emotion	0.5	0.5	0	1
Behavior	0.5	0.5	0	1
Thought	0.5	0.5	0	1
Feeling	0.5	0.5	0	1
Perception	0.5	0.5	0	1
Attention	0.5	0.5	0	1
Intuition	0.5	0.5	0	1
Imagination	0.5	0.5	0	1
Reasoning	0.5	0.5	0	1
Logic	0.5	0.5	0	1
Analysis	0.5	0.5	0	1
Synthesis	0.5	0.5	0	1
Comparison	0.5	0.5	0	1
Classification	0.5	0.5	0	1
Organization	0.5	0.5	0	1
Planning	0.5	0.5	0	1
Problem Solving	0.5	0.5	0	1
Decision Making	0.5	0.5	0	1
Communication	0.5	0.5	0	1
Interpersonal Skills	0.5	0.5	0	1
Teamwork	0.5	0.5	0	1
Leadership	0.5	0.5	0	1
Management	0.5	0.5	0	1
Organization Skills	0.5	0.5	0	1
Time Management	0.5	0.5	0	1
Resource Management	0.5	0.5	0	1
Conflict Resolution	0.5	0.5	0	1
Stress Management	0.5	0.5	0	1
Emotional Regulation	0.5	0.5	0	1
Self-Motivation	0.5	0.5	0	1
Goal Setting	0.5	0.5	0	1
Planning Skills	0.5	0.5	0	1
Problem Solving Skills	0.5	0.5	0	1
Decision Making Skills	0.5	0.5	0	1
Communication Skills	0.5	0.5	0	1
Interpersonal Skills Skills	0.5	0.5	0	1
Teamwork Skills	0.5	0.5	0	1
Leadership Skills	0.5	0.5	0	1
Management Skills	0.5	0.5	0	1
Organization Skills Skills	0.5	0.5	0	1
Time Management Skills	0.5	0.5	0	1
Resource Management Skills	0.5	0.5	0	1
Conflict Resolution Skills	0.5	0.5	0	1
Stress Management Skills	0.5	0.5	0	1
Emotional Regulation Skills	0.5	0.5	0	1
Self-Motivation Skills	0.5	0.5	0	1
Goal Setting Skills	0.5	0.5	0	1
Planning Skills Skills	0.5	0.5	0	1
Problem Solving Skills Skills	0.5	0.5	0	1
Decision Making Skills Skills	0.5	0.5	0	1
Communication Skills Skills	0.5	0.5	0	1
Interpersonal Skills Skills Skills	0.5	0.5	0	1
Teamwork Skills Skills	0.5	0.5	0	1
Leadership Skills Skills	0.5	0.5	0	1
Management Skills Skills	0.5	0.5	0	1
Organization Skills Skills Skills	0.5	0.5	0	1
Time Management Skills Skills	0.5	0.5	0	1
Resource Management Skills Skills	0.5	0.5	0	1
Conflict Resolution Skills Skills	0.5	0.5	0	1
Stress Management Skills Skills	0.5	0.5	0	1
Emotional Regulation Skills Skills	0.5	0.5	0	1
Self-Motivation Skills Skills	0.5	0.5	0	1
Goal Setting Skills Skills	0.5	0.5	0	1
Planning Skills Skills Skills	0.5	0.5	0	1
Problem Solving Skills Skills Skills	0.5	0.5	0	1
Decision Making Skills Skills Skills	0.5	0.5	0	1
Communication Skills Skills Skills	0.5	0.5	0	1
Interpersonal Skills Skills Skills Skills	0.5	0.5	0	1
Teamwork Skills Skills Skills	0.			